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Duffy, Patricia

Saturday, March 31, 2007 11:32 AM

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IN RE:10/063,546

SPDI search SEQ ID NO:38 commercial and interference.

Thanks.

Patricia A. Duffy, Ph.D. Primary Patent Examiner 571-272-0855, Remsen 3B05, Mailbox: 3C18

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Q42159 PETMA
Q70347 LUMRU
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Q91K15 ANGA
Q4248 TETING
Q16LRO AEDDAE
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Q51Y40_MAYDE
Q51Y40_DROWE
Q81Q10_DROWE
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Q81Q10_DROWE
Q81Q10_MOUSE
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JP14 HUMAN
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PRELIMINARY; PRT;
Q5JP11;
Q5JP11;
15-FEB-2005, integrated into UniProti
15-FEB-2005, sequence version 1.
02-MAY-2006, entry version 7.
Hypothetical protein DKFZp667H2312.
Name=DKFZp667H2312;
                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
SEQUENCE
Homo sapiens (Human).
Eukaryota; Metazoa; Cho
Mammalia; Eutheria; Eua
Catarrhini; Hominidae;
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Similarity 100.0%;
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PS01186; E
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720 AA;
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; EGF 2; 1.
; EGF 3; 1.
; SUSHI; 2.
; TRYPSIN DOM;
a; 80199 MW;
      Chordata; Craniata; Vertebrata; Euarchontoglires; Primates; Hapl
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Pred. No. 3.8e-288;
; Mismatches 0;
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EMBL; ALB3239; CA146203.1; -; mRNA.

Ensembl; ENSG0000149909; Homo sapiens.
GO; GO:0004252; F:serine-type endopeptidase act
GO; GO:0006508; p:proteolysis; IEA.

InterPro; IPR000859; CUB.

InterPro; IPR000712; EGF 3.

InterPro; IPR000712; EGF 3.

InterPro; IPR000712; EGF 3.

InterPro; IPR001303; EGF 11ke.

InterPro; IPR001304; Peptidase S1.S6.

InterPro; IPR001314; Peptidase S1.S6.

INTERPRO; IPR001315; CUB; 1.

Pfam; PF00084; SUSHi; 2.

PFAMRT; SM000181; EGF; 1.

SMART; SM000181; EGF; 1.

SMART; SM00181; EGF; 1.

PROSITE; PS01180; CUB; 1.

PROSITE; PS01180; CUB; 1.

PROSITE; PS01180; EGF 1; 1.

PROSITE; PS01240; TRYPSIN_DOM; 1.

PROSITE; PS04040; TRYPSIN_DOM; 1.
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The German cDNA Consortium;
Koehrer K., Beyer A., Mewes
Fobo G., Han M., Wiemann S.;
Submitted (JAN-2005) to the
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kt Local Similarity
ches 719; Conserva
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                                                       NGRHAKIGTVVSFFCNNSYVLSGNEKRTCQQNGEWSGKQPICIKACREPKISDLVRRRVL
                                                                                                                                SSPCFHDGTCVLDKAGSYKCACLAGYTGQRCENLLEERNCSDPGGPVNGYQKITGGPGLI
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PMQVQSRETPLHQLYSAAFSKQKLQSAPTKKPALPFGDLPMGYQHLHTQLQYECISPFYR
                                                                                                                                                                                                             YVEVRDGDNRDGQIIKRVCGNERPAPIQSIGSSLHVLFHSDGSKNFDGFHAIYEEITACS
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the Creative Commons Attribution-Noberivs License
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Pred. No. 7.7e-288;
1; Mismatches 0;
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GO: GO:0004252; F:serine-type endopeptidase ac

GO: GO:0006508; P:proteolysis; IEA.

InterPro; IPR00059; CUB.

InterPro; IPR006209; EGF.

InterPro; IPR006710; EGF.

InterPro; IPR006709; EGF-like_reg.

InterPro; IPR013032; EGF-like_reg.

InterPro; IPR013032; EGF-like_reg.

InterPro; IPR013032; EGF-like_reg.

InterPro; IPR001314; Peptidase_S186.

InterPro; IPR001314; Peptidase_S18.

InterPro; IPR001314; Peptidase_S18.

InterPro; IPR001314; Peptidase_S18.
Pfam; PF00431; CUB; 1.
Pfam; PF00008; EGF; 1.
Pfam; PF000084; Sushi; 2.
Pfam; PF00089; Trypsin; 1.
PRINTS; PR00722; CHYMOTRXPSIN.
SMART; SM00032; CUB; 1.
SMART; SM00032; CUB; 1.
SMART; SM000181; EGF; 2.
SMART; SM00020; Tryp SPC; 1.
PROSITE; PS01180; CUB; 1.
PROSITE; PS01180; CUB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-JUL-2004, integrated into UniProtl 05-JUL-2004, sequence version 1. 02-MAY-2006, entry version 14. Hypothetical protein DKFZp686N24154. Name=DKFZp686N24154; Homo sapiens (Human).
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The German cDNA Consortium;
Koehrer K., Beyer A., Mewes H.W., Weil B., Amid
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Q6N062;
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NCBI_TaxID=9606;
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QSEBL7;
QSEBL7;
15-MAR-2005, integrated into UniProtKB/TrEMBL.
15-MAR-2005, sequence version 1.
18-APR-2006, entry version 10.
Regeneration associated muscle protease, isoform
Name=DKFZP566H2123;
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebra
Eukaryota; Metazoa; Chordata; Craniata; Primates;
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Best Local Similarity
Matches 718; Conserv
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PROSITE; PS50026; EGF 3; 1.
PROSITE; PS50923; SUSHI; 2.
PROSITE; PS50240; TRYPSIN_DOM;
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    Catarrhini; Hominidae;
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                                                                                                                                                                                                                                                                                                                                                    CTAETGGIAAVSFPGRASPEPRWHLMGLVSWSYDKTCSHRLSTAFTKVLPFKDWIERNMK
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ilarity 99.7%;
Conservative
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Pred. No. 1.8e
1; Mismatches
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                          a; Vertebrata; Euteleos
Primates; Haplorrhini;
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720

660 660 600 600

540

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420

480

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RC TISSUB-Chondrosarcoma Lung Metastasis;
RC MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Gares L., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Romstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Raha S.S., Loquellano N.A., Peters G.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gabbs R.A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
"Generation and initial analysis of more than 15,000 full-length human
The Monne CDNA semmences.":
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                                      Query Match
Best Local Sim
Matches 720;
                                                                                                                                                 GO; GO:0008233; F:peptidase activity; II
GO; GO:0004252; F:serine-type endopeptid
GO; GO:0006508; P:proteolysis; IEA.
InterPro; IPR000859; CUB.
InterPro; IPR000859; CUB.
InterPro; IPR0006209; EGF_1ike.
InterPro; IPR006209; EGF_1ike.
InterPro; IPR006209; EGF_1ike.
InterPro; IPR001303; EGF_1ike_reg.
InterPro; IPR001303; EGF_1ike_reg.
InterPro; IPR001254; Peptidase_S1A.
InterPro; IPR001254; Peptidase_S1A.
InterPro; IPR001314; Peptidase_S1A.
InterPro; IPR001314; Peptidase_S1A.
InterPro; IPR001314; Peptidase_S1A.
InterPro; IPR001314; Peptidase_S1A.
InterPro; IPR00131; CUB; 1.
Pfam; PP000431; CUB; 1.
Pfam; PP00084; Sushi; 2.
SMART; SM00012; CUB; 1.
SMART; SM00012; CUB; 1.
SMART; SM00012; CUB; 1.
PROSITE; PS01186; EGF_2; 1.
PROSITE; PS01186; EGF_3; 1.
PROSITE; PS50236; EGF_3; 1.
PROSITE; PS50236; TRYPSIN_DOM; 1.
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Ensembl;
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Director MGC Project;
Submitted (FEB-2005) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Copyrighted Distributed
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GO:0008233; F:peptidase activity; IEA. GO:0004252; F:serine-type endopeptidase GO:0006508; P:proteolysis; IEA.
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MELGCWTQLGLTFLQLLLISSLPREYTVINEACPGAEWNIMCRECCEYDQIECVCPGKRE
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                                      Conservative
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                                                                                                                                               TRYPSIN_DOM;
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                                                                                                                   81943 MW;
                                                        99.5%;
97.7%;
                                    0;
                                  Score 3926.5;
Pred. No. 9.8e
0; Mismatches
                                                                                                                   FD3BACCFE47778FE CRC64;
                                                      8e-287;
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Q96JW2;
Q1-DEC-2001, integrated into UniProtKB/TrEMBL.
Q1-DEC-2001, sequence version 1.
Q1-DEC-2006, entry version 25.
CDAMY-2006, entry version 25.
CDNA FLJ14935 fis, clone PLACE1009992, weakly similar to LIMULUS CLOTTING FACTOR C (EC 3.4.21.84).
TISSUE=Placenta;
PubMed=14702039; DOI=10.1038/ng1285;
Ota T., Sugiyama T., Irie R.,
Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
                                                                                                                       Mammalia; Eutheria; Euc
Catarrhini; Hominidae;
                                                                                                                                                 Eukaryota; Metazoa;
                                                                                                                                                                Homo sapiens (Human)
                                                                           NUCLEOTIDE SEQUENCE
                                                                                                       NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                             HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WQAAIYRRTSGVHDGSLHKGAWFLVCSGALVNERTVVVAAHCVTDLGKVTMIKTADLKVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QHLHTQLQYECISPFYRRLGSSRRTCLRTGKWSGRAPSCIPICGKIENITAPKTQGLRWP
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                                                                                                                                   Euarchontoglires;
                                                                                                                                                   Chordata; Craniata; Vertebrata;
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                                                                                                                                                                                                                                                                                                                                                             720
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                                                                                                                                    Haplorrhini;
                                                                                                                                                    Euteleostomi;
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RA Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahari K.,
RA Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A.,
RA Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
RA Takahashi M., Kanda K., Yokoi T., Puruya T., Kikkawa E., Omura Y.,
RA Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamazaki M.,
RA Ninomiya K., Ishibashi T., Yamashita H., Murakawa K., Pujimori K.,
RA Ono Y., Takiguchi S., Watanabe M., Hiraoka S., Chiba Y., Ishida S.,
RA Chibar Y., Watanabe M., Hiraoka S., Chiba Y., Ishida S.,
RA Moriya S., Komai F., Hara R., Takeuchi K., Arita M., Imose N.,
RA Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,
RA Moriya S., Komai F., Hara R., Takeuchi K., Arita M., Imose N.,
RA Moriya S., Momiyama H., Ichihara T., Shiohata N., Sano S.,
RA Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,
RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
RA Pujinori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,
RA Ono T., Yamada K., Fuji Y., Ozaki K., Hirao M., Ohnori Y.,
RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,
RT "Complete sequencing and characterization of 21,243 full-length human
RT CDNAg: ".
                                                                                                                                                                         Query Match
Best Local Sim
Matches 719;
                                                                                                                                                                                                                                                                           Pfam; PF00431; CUB; 1.
Pfam; PF00084; SuShi; 2.
Pfam; PF00084; SuShi; 2.
Pfam; PF00089; Trypsin; 1.
Pfam; PF00089; Trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM00042; CUP; 2.
SMART; SM00042; CUB; 1.
SMART; SM000181; EGF; 2.
SMART; SM00181; EGF; 2.
SMART; SM00181; EGF; 1.
PROSITE; PS01180; CUB; 1.
PROSITE; PS01186; EGF—2; 1.
PROSITE; PS01186; EGF—2; 1.
PROSITE; PS01186; EGF—2; 1.
PROSITE; PS01186; EGF—3; 1.
PROSITE; PS0026; EGF 1; 1.
PROSITE; PS0026; EGF 3; 1.
PROSITE; PS0026; TRYPSIN DOM; 1
SEQUENCE 737 AA; 81953 MM; 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR000859; CUB.
InterPro; IPR006210; EGF:
InterPro; IPR000742; EGF:
InterPro; IPR000742; EGF:
InterPro; IPR0013032; EGF:
InterPro; IPR013032; EGF:
InterPro; IPR001303; Pept Ser Cys.
InterPro; IPR001254; Peptidase S1 S6.
InterPro; IPR001314; Peptidase S1A.
InterPro; IPR001436; Sushi_SCR_CCP.
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GO; GO:0006508; P:proteolysis;
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                                                                                                                                                                                                     Similarity
           VVGYTIPCCRNEENECDSCLIHPGCTIFENCKSCRNGSWGGTLDDFYVKGFYCAECRAGW 120
                                                                                              MELGCWTQLGLTFLQLLLISSLPREYTVINEACPGAEWNIMCRECCEYDQIECVCPGKRE
                                                                MELGCWTQLGLTFLQLLLISSLPREYTVINEACPGAEWNIMCRECCEYDQIECVCPGKRE
                                                                                                                                                                            Conservative
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                                                                                                                                                                    Score 3921.5; DB 2; Pred. No. 2.3e-286; 0; Mismatches 1;
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4F51689C5EB32B44 CRC64;
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QSRDI1 PONPY
QSRDI1;
DONPY
ID QSRDI1;
DT 21-DEC-2004, integrated into UniProtKB/TrEMBL.
DT 21-DEC-2004, sequence version 1.
DT 21-DEC-2006, entry version 8.
DT 02-MAY-2006, entry version 8.
DE Hypothetical protein DKFZp468N1810.
Mame=DKFZp468N1810;
OS Pongo pygmaeus (Orangutan).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrat OC Mammalia; Eutheria; Euarchontoglires; Primates; 1 CC (Catarrhini; Hominidae; Pongo.
NCBI TaxID=9600;
RN [1] TAXID=9600;
RN [1] The German cDNA Consortium;
RG The German cDNA Consortium;
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                                                                                                                                                                                                                                                                                                                                   Name Pysical (Orangutan).
Pongo pygmaeus (Orangutan).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Primates; Haplorrhini;
                                                                                                         The German cDNA Consortium,
Ottenwaelder B., Obermaier B., Deutschenbaur S., Schaipp
Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M
Submitted (NOV-2004) to the EMBL/GenBank/DDBJ databases.
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                                    Consortium, see http://www.uniprot.org/terms
ive Commons Attribution-NoDerivs License
                                                                                                                                  , Schaipp A.
G., Han M.,
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InterPro; IPRO00859; CUB.
InterPro; IPRO006210; EGF 1.
InterPro; IPRO006209; EGF 1.
InterPro; IPRO06209; EGF 1.
InterPro; IPRO01303; EGF 1.
InterPro; IPRO01303; EGF 1.
InterPro; IPRO01314; Peptidase s:
InterPro; IPRO01314; Peptidase s:
InterPro; IPRO01314; Peptidase s:
InterPro; IPRO0131; CUB; 1.
Pfam; PF00004; EGF; 1.
Pfam; PF00004; EGF; 1.
Pfam; PF00008; EGF; 1.
Pfam; PF00008; Trypsin; 1.
PFAM; PF00089; Trypsin; 1.
PRART; SM00101; CUB; 1.
SMART; SM00101; EGF; 2.
SMART; SM00101; EGF; 2.
SMART; SM00101; EGF; 1.
PROSITE; PS01186; EGF 1; 1.
PROSITE; PS01186; EGF 1; 1.
PROSITE; PS01186; EGF 3; 1.
PROSITE; PS01186; EGF 3; 1.
PROSITE; PS01026; EGF 3; 1.
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larity 98.5%;
Conservative
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EMBL; BT020875; AAXO8892.1; -, mRNA.

Unidene; Bt.6021; -.

MEROPS; S01.998; -.

GO; GO:000823; F:peptidase activity; IE

GO; GO:000823; F:peptidase activity; IE

GO; GO:0004252; F:serine-type endopeptid

InterPro; IPR006209; EGF

InterPro; IPR001042; EGF 3.

InterPro; IPR001032; EGF—like_reg.

InterPro; IPR001034; Peptidase_S1_S6.

InterPro; IPR001134; Peptidase_S1_S6.

InterPro; IPR001134; Peptidase_S1_S6.

InterPro; IPR001134; Peptidase_S1_S6.

InterPro; IPR00134; Sushi_SCR_CCP.

Pfam; PF00008; ITYPSin; 1.

Pfam; PF00008; EGF; 1.

Pfam; PF00008; EGF; 1.

Pfam; PF00089; TTYPSin; 1.

PRINTS; PR00122; CHYMOTRYPSIN.

SMART; SM000042; CUB; 1.

SMART; SM000042; CUB; 1.

SMART; SM000042; TYPD_SPC; 1.

PROSITE; PS01180; CUB; 1.
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SP5 BOVIN

DESPP5 BOVIN

DESPP5;

15-MAR-2005, integrated i

15-MAR-2006, sequence ver

18-APR-2006, entry versio

Regeneration associated m

Name=DKFZP556H2123;
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Eukaryota; Metazoa; Chordat
Mammalia; Eutheria; Laurasi
Pecora; Bovidae; Bovinae; E
NCBI TaxID=9913;
[1]
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MEDLINE=21180013; PubMed=11282978; DOI=10.1101/gr.170101;
MEDLINE-21180013; PubMed=11282978; DOI=10.1101/gr.170101;
Smith T.P. L., Grosse W.M., Freking B.A., Roberts A.J., Stone R.,
Casas E., Wray J.E., White J., Cho J., Fahrenkrug S.C., Bennett
Heaton M.P., Laegreid W.W., Rohrer G.A., Chitko-McKown C.G.,
Pertea G., Holt I., Karamycheva S., Liang F., Quackenbush J.,
Pertea G., Holt I., Keele J.W.;
Keele J.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Copyrighted by the Distributed under
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-Pooled;
Harhay G.P., Sonstegard T
Snelling W.M., Weidmann R
"Sequencing and analysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUCLEOTIDE
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ne; Bt.6021; -...
%; S01.998; -...
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Laurasiatheria;
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1 R.T., Sm
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T.P.L.;
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Best Local :
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QBBU25;
QBBU25;
Q1-MAR-2003, integrated into U
01-MAR-2003, sequence version:
18-APR-2006, entry version: 27.
2 days neonate thymus thymic of
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SEQUENCE
   domain, Sushi domai
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PS01186;
PS50026;
PS50923;
PS50240;
                            eonate thymus thymic cells cDNA, RIKEN clone:E430002G05 product:hypothetical Sushi domain / SCR repeat / CCP module
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EGF 2; 1.
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SUSHI; 2.
TRYPSIN_DOM;
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RX PubMed-16.41072; DOI=11.1206/science.1112014;
RA Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
RA Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
RA Davis M.J., Wilming L.G., Aidinis V., Allen J.E.,
RA bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,
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RA Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,
RA Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,
RA Ambesi-Impiombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,
RA Ambesi-Impiombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,
RA Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,
Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,
di Bernardo D., Down T., Engstrom P., Fagiolini M., Faulkner G.,
RA Clutterbuck D., Down T., Engstrom P., Fagiolini M., Faulkner G.,
RA Fletcher C.F., Fukushima T.R., Gojobori T., Green R.E.,
RA Georgi-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,
RA Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,
RA Hill D., Huminiecki L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,
RA Gortino H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,
RA Kurochkin I. V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,
Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,
RA Kutano H., Katuzawa S., Miki H., Mignone F., Miyake S., Morris K.,
RA Matsuda F., Nishider N., Nakano N., Nakauchi H., Ng P.,
RA Nishida S., Schiguchi S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,
RA Nishon R., Van Nimwegen E., Verardo R., Wei C.L., Yagi K.,
RA Tammoja K., Tan S.L., Tang S., Taylor M.S., Tener J., Teichmann S.A.,
RA Gusta R., Van Nimwegen E., Verardo R., Wei C.L., Yagi K.,
RA Grimmod S.M., Tans S., Taylor M.S., Tener J., Teichmann S.A.,
RA Grimod S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,
RA Grimod S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,
RA Grimod S., Kanamori-Katayama M., Suzuki M., Nakano K., Ninomiya N.,
Ra
                                                                                                                                                                                                                                                                      AUCLEOTIDE SEQUENCE.
STRAIN=NOD; TISSUE=Thymus;
STRAIN=NOD; TISSUE=Thymus;
PubMed=16141073; DOI=10.1126/science.1112009;
PubMed=16141073; DOI=10.1126/science Group, and Genome Scien RIKEN Genome Exploration Research Group, and Genome Scien (Genome Network Core Team) and the FANTOM Consortium;
"Antisense Transcription in the Mammalian Transcriptome."
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STRAIN=NOD, TISSUE=Tnymus;
MEDLINE=99279253; PubMed=10349636; DOI=10.10.
Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Mathods Enzymol. 303:19-44(1999).
NUCLEOTIDE SEQUENCE.
STRAIN-NOD; TISSUB-Thymus;
MEDLINE=2354663; PubMed=12466851; DOI=10.1038/nature01266;
MEDLINE=2354663; PubMed=12466851; DOI=10.1038/nature01266;
Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.
Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori
Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
Schriml L.M., Kanapin A., Matsuda H., Battalov S., Beisel K.W.,
Schriml L.M., Kanapin A., Brusic V., Chothia C., Corbani L.E., Cousins
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Mammalia; Eutheria; Euarchontoglires;
Muroidea; Muridae; Murinae; Mus.
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Euarchontoglires; Glires; Rodentia; Sciurogna
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                                                                                                                                                                    STRAIN-NOD, TISSUE-Thymus;

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Nature 409:685-690(2001).
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Pfam; PF000084; Trypsin; 1.
Pfam; PF000089; Trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM00032; CCP; 2.
SMART; SM00042; CUB; 1.
SMART; SM00181; EGF; 2.
SMART; SM00180; CUB; 1.
PROSITE; PS01180; CUB; 1.
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Ensembl; ENSMUSG00000027188; Mus Ensembl; MGI:2445082; E430002005Rik.
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                                                      YVEVRDGDNRDGQIIKRVCGNERPAPIQSIGSSLHVLFHSDGSKNFDGFHAIYEBITACS
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Furuno M.,
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F:trypsin activity; RCA.
P:proteolysis; RCA.
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Hanagaki T., Hara A
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3; Mismatches 38;
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RX MISTALINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Alteschul S.F., Zeebberg B., Buetcow K.H., Schaefer C.F., Bhat N.K.,

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RA Hopkins R.F., Jordan H., Moore T., Wang J., Hsieh F.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Stapleton M.J., Usdin T.B., Toshiki S., Carninci P., Prange C.,

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RA Romstein M.J., Medlan N.B., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Richards S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hullyk S.W.,

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RA Richards S., Worley N.C., Hale S., Garcia A.M., Gay L.J., Hullyk S.W.,

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RA Richards S., Worley A.C., Shevchenko Y., Bouffard G.G.,

RA Haltesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

"Generation and initial analysis of more than 15,000 full-length human

"Generation and initial analysis of more than 15,000 full-length human

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01-OCT-2002, integrated into Unii
01-OCT-2002, sequence version 1.
18-APR-2006, entry version 25.
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Best Local S
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Pfam; PF00089; Trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM00032; CCP; 2.
SMART; SM00032; CUB; 1.
SMART; SM00042; CUB; 1.
SMART; SM00020; Tryp SPC; 1.
PROSITE; PS01180; CUB; 1.
PROSITE; PS01186; EGF 1; 1.
PROSITE; PS01186; EGF 2; 1.
PROSITE; PS01186; EGF 3; 1.
PROSITE; PS01062; EGF 3; 1.
PROSITE; PS01086; EGF 3; 1.
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InterPro;
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GO; GO:0005615; C:extracellular space; RCA.
GO; GO:0004263; F:chymotrypsin activity; RCA.
GO; GO:0004295; F:trypsin activity; RCA.
GO; GO:0006508; P:proteolysis; RCA.
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Director MGC Project
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0; IPR000859; CUB.
0; IPR000210; EGF_1;
0; IPR000742; EGF_1;
0; IPR013032; EGF_1;
0; IPR013032; EGF_1;
0; IPR013033; Pept_Ser_Cys.
0; IPR001254; Pept; Esr_Ser_Cys.
0; IPR001314; Pept; Edase_S1A.
0; IPR0001314; Sushi_SCR_CCP.
                                                                                                                                                                                                                                                                                                                  Similarity
NERHVKIGTVVSFFCNGSYVLSGNEKRTCQQNGEWSGKQPVCMKACREPKISDLVRRRVL
              NGRHAKIGTVVSFFCNNSYVLSGNEKRTCQQNGEWSGKQPICIKACREPKISDLVRRRVL
                                                              SSPCFHDGTCVLDKAGSYKCACLAGYTGQRCENLLEERNCSDPGGPVNGYQKITGGPGLI
                                                                                                YGGDCMRCGQVLRASKGQILLESYPLNAHCEWTIHARPGFIIQLRFGMLSLEFDYMCQYD
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                                                                                                                                                                                                     VVGYTIPCCRNEDNECDSCLIHPGCTIFENCKSCRNGSWGGTLDDFYVKGFYCEECRAGW
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                                                                                                                                                                                                                                                    MELDRWAQLGLVFLQLLLISSLPREYTVINEACPGAEWNIMCRECCEYDQIECLCPGKKE
                                                                                                                                                                                                                                                                   MELGCWTQLGLTFLQLLLISSLPREYTVINEACPGAEWNIMCRECCEYDQIECVCPGKRE
                                               SSPCFHDGTCLLDTTGSFKCACLAGYTGQRCENLLEERNCSDLGGPVNGYKKITEGPGLL
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Creative Commons
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                                                                                                                                                                                                                                                                                                                 Score 3612;
Pred. No. 4
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Attribution-NoDerivs License
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RP NUCLEOTIDE SEQUENCE.

RC TISSUE=Whole body;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RX MEDLINE=22388257; Peingold E.A., Grouse L.H., Derge J.G.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RI Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

RA Wiltalon D.K., Touchman J.W., Green E.D., Dickson M.C.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

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RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Rodriguez A.C., Grimwood J., Schmutz J.M., Marra M.A.;

RA Rodriguez A.C., Grimwood J., S
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Q6DIV5;
16-AUG-2004,
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NCBI TaxID=8364;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MGC89196 protein.
Name=MGC89196;
                                                                                                                          Klein S., Gerhard D.S.;
Submitted (JUN-2004) to the
                                                  Copyrighted by the UniProt Consortium, Distributed under the Creative Commons
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                                                                                                                                                       Ole body;
Gerhard I
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                                                                                                                            EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                UniProtKB/TrEMBL
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Attribution-NoDerivs License
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R Ensembl; ENSXETGO000007554; Xenopus tropicalis.

R GO; GO:0004252; F:serine-type endopeptidase activity; IEA

R GO; GO:000508; p:proceolysis; IEA.

R InterPro; IPR000509; CUB.

R InterPro; IPR000742; EGF_3.

R InterPro; IPR000742; EGF_1ike.

R InterPro; IPR000742; EGF_1ike_reg.

InterPro; IPR0000742; EGF_1ike_reg.

InterPro; IPR001032; Pept_Ser_Cys.

R InterPro; IPR001034; Sushi_SCR_CCP.

R InterPro; IPR000145; Sushi_SCR_CCP.

R Ffam; PP00008; EGF; 1.

R Pfam; PP00008; EGF; 1.

R PACSITE; PS01180; CUB; 1.

R PROSITE; PS01180; CUB; 1.

R PROSITE; PS01180; CUB; 1.

R PROSITE; PS01180; EGF_2; 1.

R PROSITE; PS0126; EGF_3; 1.

R PROSITE; PS02026; EGF_3; 1.

R PROSITE; PS0223; SUSHi; 2.

R PROSITE; PS02240; TRYPSIN_DOM; 1.

SEQUENCE 722 AA; 80367 NM; F173563206D1AE82 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MELGCWTQLGLTFLQLLLISSLP--REYTVINEACPGAEWNIMCRECCEYDQIECVCPGK
                                                                                                                                                                                                                                                                                                                                                         VLPMQVQSRETPLHQLYSAAFSKQKLQSAPTKKPALPFGDLPMGYQHLHTQLQYECISPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NOKVGYTIPCCRNEENECDSCLIHPGCSIFENCKSCNNGSWGGTLDDFYIKGSYCSECRM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REVVGYTIPCCRNEENECDSCLIHPGCTIFENCKSCRNGSWGGTLDDFYVKGFYCAECRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MALLVWSSLVVASLHLLGTAAYPSRSKYTVINENCPGAEWNIMCRDCCEYDQVECACPDG
                                                                                                                                                                               SLHKGAMFLVCSGALVNERTVVVAAHCVTDLGKVTMIKTADLKVVLGKFYRDDDRDEKTI
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                                                                                                                                                 SLRKGSWYLVCSGALLNERTVVMAAHCVTDLGKSSIIKVSDMKVVLGKFYRDDDREEKSQ
                                                                                                                                                                                                                                                         YRRTGSSRRTCLKTGKWSGRAPSCIPICGKLENFNITQLGEQRWPWQAALYRRSNGVKDA
                                                                                                                                                                                                                                                                                    YRRLGSSRRTCLRTGKWSGRAPSCIPICGKIENITAPKTQGLRWPWQAAIYRRTSGVHDG
AGWNVLADVRSPGFKNDTLRSGVVSVVDSLLCEEQHEDHGI PVSVTDNMFCASWEPTAPS
                                               QHLHISAVIVNPNYDPILLDSDIAVIKLLDKARVSDYVQPVCLTLATEMITSPQBYTIVI
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66.9%;
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0; Mismatches
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RESULT 11
Q711RB9 HUWAN
ID Q711RB9 HUWAN
AC Q71RB9;
DT 05-JUL-2004, s
DT 18-APR-2006, c
DE FP938.
OS Homo sapiens (OC Eukaryota; Met
OC Eukaryota; Met
OC Mammalia; Eutl
OC Catarrhini; He
OX NCBI_TaxID=966
RN NUCLEOTIDE SEC
RN NU
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Best Local (
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Pfam; PF00089; Trypsin; 1.

PRINTS; PR00725; CHYMOTRYPSIN.

SMART; SM00020; Tryp_SPC; 1.

PROSITE; PS50923; SUSHI; 1.

PROSITE; PS50240; TRYPSIN Dow; 1

Serine protease homolog; Sushi.

SEQUENCE 417 AA; 46703 MW; 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ensembl; ENSG00000149090; Homo sapiens.
GO; GO:0004252; F:serine-type endopeptidase
GO; GO:0004508; P:proceolysis; IEA.
InterPro; IPR009003; Pept Ser_Cys.
InterPro; IPR001254; Peptidase_S1A.
InterPro; IPR001314; Peptidase_S1A.
InterPro; IPR001314; Sushi_SCR_CCP.
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Wan D.F., Gu J.R.;
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Belongs to the peptidase S1 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-JUL-2004, integrated into UniProtKB/TrEMBL 05-JUL-2004, sequence version 1.
18-APR-2006, entry version 12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
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Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
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                                                                                                                                                                                                        KWSGRAPSCIPICGKIENITAPKTQGLRWPWQAAIYRRTSGVHDGSLHKGAWFLVCSGAL
                                                                                                                                                                                                                                                                                                                                                LYSAAFSKQKLQSAPTKKPALPFGDLPMGYQHLHTQLQYECISPFYRRLGSSRRTCLRTG
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                                                                                                                                                                                                                                                                                                    LYSAAFSKOKLOSAPTKKPALPFGDLPMGYQHLHTQLQYECISPFYRRLGSSRRTCLRTG
                                                                                                                                                                                                                                                                                                                                                                                                                                     FVTTPMFLVAMRKELASRMERWSGKQPICIKACREPKISDLVRRRVLPMQVQSRETPLHQ
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                                        VNERTVVVAAHCVTDLGKVTMIKTADLKVVLGKFYRDDDRDEKTIQSLQISAIILHPNYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              52.2%;
95.6%;
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Pred. No. 2
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RASULT 12
Q4SAF4 TETING
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RA Jaillon O., Aury J.-M., Brunet F., Petit J.-L., Stange-Thomann N.,
RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Micaud S., Jaffe D., Fischer S., Lutfalla G., Dossat C., Segurens B.,
RA Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
Anthouard V., Jubin C., Cattelli V., Katinka M., Vacherie B.,
RA Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
RA Cruaud C., Duprat S., Brottier P., Coutanceau J.-P., Gouzy J.,
RA Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
RA Rellis M., Volff J.-N., Guigo R., Zody M.C., Mesirov J.,
RA Kellis M., Volff J.-N., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
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RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Mincker P., Lander E.S., Weissenbach J., Roest Crollius H.;
"Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RT The early vertebrate proto-karyotype.";
Nature 431:946-957(2004).
                                                                                           GO; GO:0004252; F:serine-type endopepti
GO; GO:0006508; P:proteolysis; IEA.
InterPro; IPR000859; CUB.
InterPro; IPR000742; EGF 3.
InterPro; IPR000742; EGF 1ike.
InterPro; IPR001209; EGF 1ike.
InterPro; IPR001303; EGF 1ike reg.
InterPro; IPR001303; EGF 1ike S1.
InterPro; IPR001254; Peptidase S1.
InterPro; IPR001354; Peptidase S1A.
InterPro; IPR001354; Sushi_SCR_CCP.
Pfam; PF00431; CUB; 1.
Pfam; PF00038; EGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genoscope; Whitehead Institute Centre for Genome Research;
Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
-i- CAUTION; The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry whi
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Tetraodon.
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19-JUL-2005, sequence version 1.
02-MAY-2006, entry version 7.
Chromosome 13 SCAF14688, whole genome shotgun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; CAAE01014688; CAG02378.1; -; Genomic_DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Distributed under the Creative Commons
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                                  Sushi; 2.
Trypsin; 1
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SMART; SM00042; CUB; 1.

SMART; SM00020; Tryp_SPc; 1.

SMOOTTE; PS01180; CUB; 1.

PROSITE; PS01186; EGF 1; 1.

PROSITE; PS50126; EGF 2; 1.

PROSITE; PS50026; EGF 3; 1.

PROSITE; PS50026; EGF 3; 1.

PROSITE; PS50026; TRYPSIN_DOM; 1.

SEQUENCE 1009 AA; 111811 MW;
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                                                                                                                                                                      VNERTVVVAAHCVTDLGKVTMIKTADLKVVLGKFYRDDDRDEKTIQSLQISAIILHPNYD
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                                                                 DSHWPWLAAIYRRSNNRVGKKVTSGDGQTGSLKTDDGAGSGVRD----LESDWQLVCSGVL
                                                                                                                                                                                                                                  GLRWPWQAAIYRRT-----
                                                                                                                                                                                                                                                                           LPMGYQHLHTQLQYECISPFYRRLGSSRRTCLRTGKWSGRAPSCIPICGKIENITAPKTQ
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PPLTDSRTSSHRPSQGKGEDKGRWRLLGLVSFGYDQGECDPDLYTVYTHVANFKDW
                                                                                                    PHVLDSDVAVIRLLDKAKIGEKVAPLCLSDSQEDLETTSEQGLVT--GWSPVPD---PSL
                                                                                                                                                       VNORSVVVAAHCVTELGKVYPLETAKLKVVVGKHFREDOREDKGPOHLRVDSIAVHENYD
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CKSCRNGSWGGTLDDFYVKGFYCAECRAGWYGGDCMRCGQVLRAPKGQILLESYPLNAHC

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X. Jaillon O., Aury J.-M., Brunet F., Petit J.-L., Stange-Thomann N.,

AM Maucell E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,

Nanicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,

AM Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,

AM Anthouard V., Jubin C., Catolico L., Poulain J., De Berardinis V.,

Cruaud C., Duprat S., Brottler P., Coutanceau J.-P., Gouzy J.,

AM Cruaud C., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,

AM Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,

AM Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,

AM Lindblad-Toh K., Birren B., Nubbaum C., Kahn D., Robinson-Rechavi M.,

AM Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,

"Genome duplication in the teleost fish Tetraodon nigroviridis reveals

the early vertebrate proto-karyotype.";

Nature 431:946-957(2004).
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Q4SHD4;
19-JUL-2005, integrated into Un
19-JUL-2005, sequence version 1
18-APR-2006, entry version 6.
Chromosome 5 SCAF14581, whole g
                                                                                                                                                                                                                                                  InterPro; IPRO00859; CUB.
InterPro; IPRO09003; Pept Ser Cys.
InterPro; IPRO1254; Peptidase S1 S6.
InterPro; IPRO00436; Sushi_SCR_CCP.
Pfam; PP000431; CUB; 1.
Pfam; PP00084; Sushi; 1.
Pfam; PP00089; Trypsin; 1.
SMART; SM00042; CUB; 1.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;

Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;

Tetradontoidea; Tetraodontidae; Tetraodon.
                                                                                                                                   Sushi.
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Genoscope; Whitehead Institute Centre for Genome Research;
Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry whi
                                                                                                                                                                                                 PROSITE; PS01180; CUB; 1.
PROSITE; PS50923; SUSHI; 1.
PROSITE; PS50240; TRYPSIN_DOM;
                                                                                                                                                                                                                                                                                                                                                                                      EMBL; CAAE01014581; CAF99948.1; -; Genomic I
GO; GO:0004252; F:serine-type endopeptidase
GO; GO:0006508; P:proteolysis; IEA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
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SIMILARITY: Belongs to the peptidase
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                   EACPGAEWNIMCRECCEYDQIECVCPGKREVVGYTIPCCRNEENECDSCLIHPGCTIFEN
DRCPSSRWNAMCRPCCEYQLIQCRCPSKGLKVGYTVPCCRNALNQCDPCLIPPGCSLFEN
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                                                                Score 1122.5;
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                                                                                                                                    871FD09B36BD90A6 CRC64;
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                                                                                   .5; DB 2;
1.1e-75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           S1 family.
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                                                                                                                                                                                                                                                                                                                                                                                                                            DNA
                                                                  155;
                                                                                                                                                                                                                                                                                                                                                                                                         activity; IEA.
                                                                  Indels
                                                                                                Length
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Y432 HUMAN
PRELIMINARY; PRT; 181 AA.
Q9Y432;
Q9Y432;
O1-NOV-1999, integrated into UniProtKB/TrEMBL.
F 01-NOV-1999, sequence version 1.
F 01-NOV-1999, sequence version 28.
F 18-APR-2006, entry version 28.
E Hypothetical protein DKFZp586H2123 (Fragment).
N Name=DKFZp586H2123;
GO; GO:0004252; F:serine-type endopeptidase ac GO; GO:0006508; P:proteolysis; IEA.
InterPro; IPR009003; Pept Ser Cys.
InterPro; IPR001254; Peptidase S1 S6.
Pfam; PF00089; Trypsin; 1.
SMART; SM00020; Tryp SPC; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
Hypothetical protein.
NON_TER
                                                                                                                                                                                                                                                                                    EMBL; AL050214; CAB43317.1; -; mRNA.
PIR; T08805; T08805
HSSP; P00736; 1MD7.
MEROPS; S01.998; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ansorge W., Wirkner U., Mewes H.W., Gassenhuber J., Wier Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases -!- SIMILARITY: Belongs to the peptidase S1 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Euarchontoglires; Primates; Hapl
                                                                                                                                                                                                    Ensembl; ENSG00000149090;
GO; GO:0004252; F:serine-t
GO; GO:0006508; P:proteol)
                                                                                                                                                                                                                                                                                                                                                                                                                       Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Uterus;
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| LVHPDFH-FGAESNVAVLKLRDKAKISERVLPVCL
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Haplorrhini;
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SMART; SM00032; CCP; 5.

SMART; SM00034; CLECT; 1.

SMART; SM00603; LCCL; 1.

SMART; SM00603; LCCL; 1.

SMART; SM00020; Tryp_SPC; 1.

PROSITE; PS500041; C_TYPE_LECTIN_2; 1.

PROSITE; PS00022; EGF_1; UNKNOWN_1.

PROSITE; PS50020; LCCL; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR0013111; EGF 3.
InterPro; IPR013111; EGF extracel
InterPro; IPR013013; EGF like re;
InterPro; IPR001304; LCCL.
InterPro; IPR001304; Lectin C.
InterPro; IPR001304; Pept Ser Cy
                                                                                                                                                                                                                                                                                                              Pfam; PF00059;
Pfam; PF00084;
Pfam; PF00089;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MUCLEOTIDE SEQUENCE.
MEDLINE=21955715; PubMed=11958140;
MARDLINE=21955715; PubMed=11958140;
Wang D., Liu J., Chen L., Wang L., Yang G., Wu X.,
"Cloning and expression of Tachypleus tridentatus;
"Cloning and expression of Tachypleus tridentatus;
Acta Biochim. Biophys. Sin. 34:77-82(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Arthropoda; C
Limulidae; Tachyolene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QBT9S1 TACTR PRELIMINARY; PRT; 1019 AA.
QBT9S1;
QBT9S1
                                                                                                                                                                                                                                                                              Pfam; PF00059; Lectin_C; 1.
Pfam; PF000084; Sushi; 5.
Pfam; PF00089; Trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN
                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR000436; Su
Pfam; PF07974; EGF 2; 1
Pfam; PF03815; LCCL; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GO; GO:0004252; F:serine-type endop
GO; GO:0005529; F:sugar binding; IE
GO; GO:0006598; P:proteclysis; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSSP;
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; Peptidase_S1A.
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ng; IEA.
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Attribution-NoDerivs License
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PSS0240; TRYPSIN DOM; 1.
PS00134; TRYPSIN HIS; UNKNOWN 1.
PS00135; TRYPSIN SER; 1.
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                                                                                                                                                                                                                                                                                       MGYQHLHTQLQYECISPFYRRLGSSRRTCLRTGKWSGRAPSCIPICGKIENITAP-----
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                                                                                                                                                 EGHYRVGSRAIYTCESRYYELLGSQGRRCDSNGNWSGRPASCIPVCGRSDSPRSPFIWNG
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26 1019 factor C.
1019 AA; 112249 MW; BBE51730AE595993 CRC64;
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Search completed: April 4, 2007, 22:04:11 Job time: 399 secs

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Result
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APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
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                                                                                      Fong, Sherman
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Pred. No. 0;
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CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR APPLICATION NUMBER: 60/065186
PRIOR APPLICATION NUMBER: 60/065186
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR FILING DATE: 1997-11-12
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OR FILING DATE: 1998-06-05

R APPLICATION NUMBER: 60/088217

OR FILING DATE: 1998-06-05

OR FILING DATE: 1998-06-09

OR APPLICATION NUMBER: 60/088655

OR FILING DATE: 1998-06-09

OR FILING DATE: 1998-06-10

OR FILING DATE: 1998-06-10
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PR APPLICATION NUMBER: 60/088029

DR FILING DATE: 1998-06-04

PR APPLICATION NUMBER: 60/088030

DR FILING DATE: 1998-06-04

DR APPLICATION NUMBER: 60/088033

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APPLICATION NUMBER: 60/087607
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FILING DATE: 1998-06-05
APPLICATION NUMBER: 60/088202
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APPLICATION I
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Kljavin, Ivar J.
Napier, Mary A.
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art, Timothy A.
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OR FILING DATE: 1998-06-26
OR APPLICATION NUMBER: 60/091360
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OR APPLICATION NUMBER: 60/091549
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                                                                                                                       NGRHAKIGTVVSFFCNNSYVLSGNEKRTCQQNGEWSGKQPICIKACREPKISDLVRRRVL
                                                                                                                                                                                           SSPCFHDGTCVLDKAGSYKCACLAGYTGQRCENLLEERNCSDPGGPVNGYQKITGGPGLI
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RLGSSRRTCLRTGKWSGRAPSCIPICGKIENITAPKTQGLRWPWQAAIYRRTSGVHDGSL
                             PMQVQSRETPLHQLYSAAFSKQKLQSAPTKKPALPFGDLPMGYQHLHTQLQYECISPFYR
                                              PMQVQSRETPLHQLYSAAFSKQKLQSAPTKKPALPFGDLPMGYQHLHTQLQYECISPFYR
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                                                                                                 NGRHAKIGTVVSFFCNNSYVLSGNEKRTCQQNGEWSGKQPICIKACREPKISDLVRRRVL
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APPLICATION

1998-06-19 1998-06-19 1998-06-1998-06-

FILING DATE:

NESULT 3 Sequence 211 Application US/09997333 Patest No. 6653836 GENERAL INVOCAMION: APPLICANT BACKET, DAVId APPLICANT BOSECHI, DAVId APPLICANT GETTISER, MATY E. APPLICANT GETTISER, MATY E. APPLICANT GOGOWSKI, POLI J. APPLICANT MADIE: MATY A. APPLICANT MADIE: MATY A. APPLICANT MADIE: MATY A. APPLICANT MADIE: MATY A. APPLICANT MOSECHIAN, DAVIE J. APPLICANT WOOL WILLIAM I. APPLICANT WOOL WILLIAM I. APPLICANT WOOL WILLIAM I. APPLICANT WOOL WILLIAM I. APPLICANT SCHORE COLIN K. APPLICANT WOOL WILLIAM I. APPLICA	Db 421 RLGSSRRTCLRTCKWSGRAPSCIPICGKIENITAPKTQGLRWPWQAAIYRRTSGVHDGSL 480 Qy 481 HKGAWFLVCSGALVNERTVVVAAHCVTDLGKVTMIXTADLKVVLGKFYRDDRDEKTIQS 540
PRIOR APPLICATION NUMBER: 60/08/08/08/08/08/08/08/08/08/08/08/08/08	PRIOR FILING DATE: 1998-05-28 PRIOR APPLICATION NUMBER: 60/087607 PRIOR PILING DATE: 1998-06-02 PRIOR PILING DATE: 1998-06-03 PRIOR PILING DATE: 1998-06-03 PRIOR PILING DATE: 1998-06-04 PRIOR APPLICATION NUMBER: 60/088021 PRIOR PILING DATE: 1998-06-04 PRIOR PILING DATE: 1998-06-04

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PRIOR
DATE: 1398-06-25
OR APPLICATION NUMBER: 60/09
OR FILING DATE: 1998-06-25
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DR FILING DATE: 1998-06-19
DR APPLICATION NUMBER: 60/089948
DR FILING DATE: 1998-06-19
DR APPLICATION NUMBER: 60/089952
DR FILING DATE: 1998-06-19
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Sequence 231, Application Us
Patent No. 6956108
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Beststein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleo
APPLICANT: Gerber, Hanspett
APPLICANT: Gerritsen, Mary
APPLICANT: Gerritsen, Mary
APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul .

Ashkenazi, Avi J.
Baker, Kevin P.
Botstein, David
Desnoyers, Luc
Eaton, Dan L.
Ferrara, Napoleone
Fong, Sherman
Gerber, Hanspeter
Gerritsen, Mary E.
Goddard, Audrey
Godowski, Paul J.

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APPLICATION NUMBER: 60/092182
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          CTAETGGIAAVSFPGRASPEPRWHLMGLVSWSYDKTCSHRLSTAFTKVLPFKDWIERNMK
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                                                WNVLADVRSPGFKNDTLRSGVVSVVDSLLCCEQHEDHGIPVSVTDNMFCASWEPTAPSDI
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CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
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DR APPLICATION NUMBER: 60/088030

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DR APPLICATION NUMBER: 60/088033

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DR APPLICATION NUMBER: 60/088167

DR FILING DATE: 1998-06-05

DR APPLICATION NUMBER: 60/088202

DR FILING DATE: 1998-06-05

DR APPLICATION NUMBER: 60/088212

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FILING DATE: 1998-06-04
APPLICATION NUMBER: 60/08028
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APPLICATION NUMBER: 60/088029
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APPLICATION NUMBER: 60/087759
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APPLICATION NUMBER: 60/087827
FILING DATE: 1998-06-03
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APPLICATION NUMBER: 60/087607
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APPLICATION NUMBER: 60/087609
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FILING DATE: 1998-06-04
APPLICATION NUMBER: 60/088025
FILING DATE: 1998-06-04
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FILING DATE: 1998-02-25
APPLICATION NUMBER: 60/078910
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FILING DATE: 1997-11-13
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Roy, Margaret Ann
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Kljavin, Ivar J
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OR APPLICATION NUMBER: 60/089952
OR APPLICATION NUMBER: 60/090246
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OR APPLICATION NUMBER: 60/090252
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OR FILING DATE: 1998-06-24

REPLICATION NUMBER: 60/090445

RE FILING DATE: 1998-06-24

OR APPLICATION NUMBER: 60/090472

OR FILING DATE: 1998-06-24

OR APPLICATION NUMBER: 60/090535

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APPLICATION NUMBER: 60/089948
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FILING DATE: 1998-06-18
APPLICATION NUMBER: 60/089907
FILING DATE: 1998-06-18
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FILING DATE: 1998-06-11
APPLICATION NUMBER: 60/088861
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FILING DATE: 1998-06-24
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FILING DATE: 1998-06-11
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FILING DATE: 1998-06-12
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APPLICATION NUMBER: 60/088738
FILING DATE: 1998-06-10
APPLICATION NUMBER: 60/088742
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OR FILING DATE: 1998-06-24
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FILING DATE: 1998-07-01
APPLICATION NUMBER: 60/091519
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FILING DATE: 1998-06-25
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                                                                                         YGGDCMRCGQVLRAPKGQILLESYPLNAHCEWTIHAKPGFVIQLRFVMLSLEFDYMCQYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SSPCFHDGTCYLDKAGSYKCACLAGYTGQRCENLLEERNCSDPGGPVNGYQK1TGGPGLI
                                                                                                                                                                                                                      SSPCFHDGTCVLDKAGSYKCACLAGYTGQRCENLLEERNCSDPGGPVNGYQKITGGPGLI
                                                                                                                                                                                                                                                                                       YVEVRDGDNRDGQIIKRVCGNERPAPIQSIGSSLHVLFHSDGSKNFDGFHAIYEEITACS
                                                                                                                                                                                                                                                                                                                  YVEVRDGDNRDGQIIKRVCGNERPAPIQSIGSSLHVLFHSDGSKNFDGFHAIYEEITACS
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                        PMQVQSRETPLHQLYSAAFSKQKLQSAPTKKPALPFGDLPMGYQHLHTQLQYECISPFYR
                                                                                                                                                                                                                                                                                                                                                                                   YGGDCMRCGQVLRAPKGQILLESYPLNAHCEWTIHAKPGFVIQLRFVMLSLEFDYMCQYD
PMQVQSRETPLHQLYSAAFSKQKLQSAPTKKPALPFGDLPMGYQHLHTQLQYECISPFYR
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APPLICANT: WOOD, WILLIAM I.

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ITITE OF INVENTION: Acids Encoding the Same

FILE REFERENCE: P2730P1C61

CURRENT APPLICATION NUMBER: US/09/989,735

CURRENT FILING DATE: 2001-11-19

PRIOR APPLICATION NUMBER: 60/049787

PRIOR FILING DATE: 1997-10-17

PRIOR PILING DATE: 1997-10-17

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Grimaldi, J. Christopher
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Goddard, Audrey
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Botstein, David
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Williams, P. Mickey
Wood, William I.
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Stewart, Timothy A.
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; Sequence 231, Appl
; Patent No. 7018811
    GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, Javid
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napole
APPLICANT: Fong, Sherman
APPLICANT: Gerrber, Hanspet
APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey
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                                                                                                                                                                                                                                                                                                                                                                  CTAETGGIAAVSFPGRASPEPRWHLMGLVSWSYDKTCSHRLSTAFTKVLPFKDWIERNMK
                                                                                                                                                                                                                                                                                                                                                                                                                       WNVLADVRSPGFKNDTLRSGVVSVVDSLLCEEQHEDHGIPVSVTDNMFCASWEPTAPSDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LQISAIILHPNYDPILLDADIAILKLLDKARISTRVQPICLAASRDLSTSFQESHITVAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HKGAWFLVCSGALVNERTVVVAAHCVTDLGKVTMIKTADLKVVLGKFYRDDDRDEKTIQS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YGGDCMRCGQVLRAPKGQTLLESYPLNAHCEWTTHAKPGFVTQLRFVMLSLEFDYMCQYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LQISATILHPNYDPILLDADIAILKLLDKARISTRVQPICLAASRDLSTSFQESHITVAG
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                                                                                                                                                                                                                                                                                                                                             CTAETGGIAAVSFPGRASPEPRWHLMGLVSWSYDKTCSHRLSTAFTKVLPFKDWIERNMK
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Pred. No. 0;
0; Mismatches
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CURRENT FILING DATE: 1997-06-16
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PRIOR PILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065311
PRIOR PILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/06570
PRIOR PILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/06571
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PRIOR PILING DATE: 1998-05-27
PRIOR APPLICATION NUMBER: 60/08760
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PRIOR PILING DATE: 1998-06-02
PRIOR PILING DATE: 1998-06-04
PRIOR PILING DATE: 1998-06-04
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PRIOR PPLICATION NUMBER: 60/088026
PRIOR PRILING DATE: 1998-06-04
PRIOR PPLICATION NUMBER: 60/088026
PRIOR PPLICATION NUMBER: 60/088026
PRIOR PPLICATION NUMBER: 60/088029
PRIOR PRILING DATE: 1998-06-04
PRIOR PPLICATION NUMBER: 60/088029
PRIOR PRILING DATE: 1998-06-05
PRIOR PPLICATION NUMBER: 60/088020
PRIOR PRILING DATE: 1998-06-05
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APPLICANT: Grimaldi, J.Chris
APPLICANT: Grimaldi, J.Chris
APPLICANT: Kljavin, Ivar J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Roy, Margaret An
APPLICANT: Stewart, Timothy
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin
APPLICANT: Watanabe, Colin
APPLICANT: Williams, P. Mic
APPLICANT: Williams, P. Mic
APPLICANT: Wood, William I.
APPLICANT: Sang, Zemin
TITLE OF INVENTION: Secreted
TITLE OF INVENTION: Secreted
TITLE REFERENCE: P7730F1C60
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Part, Timothy
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APPLICATION

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FILING DATE: FILING DATE: APPLICATION

NUMBER: 60/088824

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1998-06-10

APPLICATION NUMBER: 60/088810

NUMBER:

60/088742

NUMBER: NUMBER:

60/088738 60/088734

APPLICATION IN FILING DATE:
APPLICATION I

APPLICATION NUMBER: 60/088876 FILING DATE: 1998-06-11 APPLICATION NUMBER: 60/089105

FILING DATE: 1998-06-11
APPLICATION NUMBER: 60/088861
FILING DATE: 1998-06-11

NUMBER: 60/088858 NUMBER: 60/088826

1998-06-10

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NUMBER: 60/089514

1998-06-16 1998-06-16

NUMBER: 60/089532

FILING DATE: 1998-06-16 APPLICATION NUMBER: 60/089512 FILING DATE: 1998-06-12 APPLICATION NUMBER: 60/089440

FILING DATE: 1998-06-17
APPLICATION NUMBER: 60/089538
FILING DATE: 1998-06-17
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FILING DATE: 1998-07-02
APPLICATION NUMBER: 60/091978
FILING DATE: 1998-07-07
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FILING DATE: 1998-07-02
APPLICATION NUMBER: 60/091544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 60/090690 FILING DATE: 1998-06-25 APPLICATION NUMBER: 60/090694 FILING DATE: 1998-06-25
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APPLICATION NUMBER: 60/090540
FILING DATE: 1998-06-24
APPLICATION NUMBER: 60/090542
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APPLICATION NUMBER: 60/091519
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FILING DATE: 1998-06-26
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FILING DATE: 1998-06-25
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FILING DATE: 1998-06-25
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APPLICATION NUMBER:
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APPLICATION NUMBER: 60/091626
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                 PMQVQSRETPLHQLYSAAFSKQKLQSAPTKKPALPFGDLPMGYQHLHTQLQYECISPFYR
                                                                                      NGRHAKIGTVVSFFCNNSYVLSGNEKRTCQQNGEWSGKQPICIKACREPKISDLVRRRVL
                                                                                                                                  SSPCFHDGTCVLDKAGSYKCACLAGYTGQRCENLLEERNCSDPGGPVNGYQKITGGPGLI
                                                                                                                                                      SSPCFHDGTCVLDKAGSYKCACLAGYTGQRCENLLEERNCSDPGGPVNGYQKITGGPGLI
                                                                                                                                                                                                   YVEVRDGDNRDGQIIKRVCGNERPAPIQSIGSSLHVLFHSDGSKNFDGFHAIYEEITACS
                                                                                                                                                                                                                     YVEVRDGDNRDGQIIKRVCGNERPAPIQSIGSSLHVLFHSDGSKNFDGFHAIYEEITACS
                                                                                                                                                                                                                                                                       YGGDCMRCGQVLRAPKGQILLESYPLNAHCEWTIHAKPGFVIQLRFVMLSLEFDYMCQYD
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                                                                                                                                                                                                                                                                                                                                                                                                                              MELGCWTQLGLTFLQLLLISSLPREYTVINEACPGAEWNIMCRECCEYDQIECVCPGKRE
PMQVQSRETPLHQLYSAAFSKQKLQSAPTKKPALPFGDLPMGYQHLHTQLQYECISPFYR
                                                             NGRHAKIGTVVSFFCNNSYVLSGNEKRTCOONGEWSGKOPICIKACREPKISDLVRRRVL
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Pred. No. 0;
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APPLICATION NUMBER: 60/ FILING DATE: 1998-06-24

APPLICATION I

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60/090444 60/090435 60/090431 60/090429 60/090355 60/090349 60/090254

1998-06-24

APPLICATION NUMBER: FILING DATE: 1998-00

1998-06-24

60/090472 60/090445

APPLICATION NUMBER:

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FILING DATE:

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1998-06-23

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1998-06-22

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60/090252 60/090246

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NUMBER: 60/089948

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60/089952

APPLICATION

1998-06-19

APPLICATION

NUMBER:

60/089947

NUMBER: 60/089908

FILING DATE:

NUMBER:

60/089907

FILING DATE:

APPLICATION NUMBER: 60/089600 FILING DATE: 1998-06-17

NUMBER: 60/089653: 1998-06-17

NUMBER: 60/089801

1998-06-18

APPLICATION APPLICATION APPLICATION : FILING DATE:

NUMBER: 60/089599

1998-06-17

FILING DATE:

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RESULT
US-09-9
CURRENT APPLICATION NUMBER: US/09/997,514
CURRENT FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065250
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-33
PRIOR APPLICATION NUMBER: 60/06670
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/075945
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PRIOR FILING DATE: 1998-03-20
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APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C46
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Kljavin, Ivar J
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Grimaldi, J. Christopher
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Gerritsen, Mary E.
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Mart, Timothy A.
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OR APPLICATION NUMBER: 60/089440
OR PILING DATE: 1998-06-16
OR APPLICATION NUMBER: 60/089512
OR FILING DATE: 1998-06-16
OR APPLICATION NUMBER: 60/089514
OR FILING DATE: 1998-06-16
OR APPLICATION NUMBER: 60/08953
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OR APPLICATION NUMBER: 60/08959
OR FILING DATE: 1998-06-17
OR APPLICATION NUMBER: 60/08959
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DR FILING DATE: 1998-05-28
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DR APPLICATION NUMBER: 60/087607
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DR FILING DATE: 1998-06-02
DR APPLICATION NUMBER: 60/087759
DR FILING DATE: 1998-06-02
DR APPLICATION NUMBER: 60/088025
DR APPLICATION NUMBER: 60/088025
DR FILING DATE: 1998-06-04
DR APPLICATION NUMBER: 60/088025
DR FILING DATE: 1998-06-04
DR APPLICATION NUMBER: 60/088026
DR FILING DATE: 1998-06-04
DR APPLICATION NUMBER: 60/088028
DR FILING DATE: 1998-06-04
DR APPLICATION NUMBER: 60/088033
DR FILING DATE: 1998-06-04
DR APPLICATION NUMBER: 60/088167
DR APPLICATION NUMBER: 60/088202
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OR FILING DATE: 1998-06-18

OR APPLICATION NUMBER: 60/089907

OR FILING DATE: 1998-06-18

OR APPLICATION NUMBER: 60/089908

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Sequence 231, Application US, Patent No. 7029873
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eacon, Dan L.
APPLICANT: Ferrara, Napoleon
APPLICANT: Ferrara, Napoleon
APPLICANT: Gerber, Hanspete)
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Fong, Sherman
Gerber, Hanspeter
Gerritsen, Mary E
                                     Eaton, Dan L.
Ferrara, Napoleone
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OR FILING DATE: 1998-06-18
OR APPLICATION NUMBER: 60/089947
OR APPLICATION NUMBER: 60/089948
OR FILING DATE: 1998-06-19
OR APPLICATION NUMBER: 60/089952
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OR APPLICATION NUMBER: 60/065186
OR FILING DATE: 1997-11-12
OR APPLICATION NUMBER: 60/065311
OR FILING DATE: 1997-11-13
OR APPLICATION NUMBER: 60/06770
OR FILING DATE: 1997-11-24
OR APPLICATION NUMBER: 60/075945
OR FILING DATE: 1998-02-25
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DR FILING DATE: 1998-06-02
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DR APPLICATION NUMBER: 60/087827
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Godowski, Paul J.
Grimaldi, J.Christopher
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Williams, P. Mickey
Wood, William I.
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Stewart, Timothy A.
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OR APPLICATION NUMBER: 60/088734
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APPLICATION NUMBER: 60/090542
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APPLICATION NUMBER: 60/090557
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APPLICATION NUMBER: 60/091982
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APPLICATION NUMBER: 60/091978
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APPLICATION NUMBER: 60/090862
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APPLICATION NUMBER: 60/090690
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APPLICATION NUMBER: 60/090676
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                                                                                                                                                                                      YVEVRDGDNRDGQIIKRVCGNERPAPIQSIGSSLHVLFHSDGSKNFDGFHAIYEEITACS
PMQVQSRETPLHQLYSAAFSKQKLQSAFTKKPALFFGDLFMGYQHLHTQLQYECISFFYR
                                                NGRHAKIGTVVSFFCNNSYVLSGNEKRTCQQNGEWSGKQPICIKACREPKISDLVRRRVL
                                                                  NGRHAKIGTVVSFFCNNSYVLSGNEKRTCQQNGEWSGKQPICIKACREPKISDLVRRRVL
                                                                                                           SSPCFHDGTCVLDKAGSYKCACLAGYTGQRCENLLEERNCSDPGGPVNGYQKITGGPGLI
                                                                                                                                 SSPCFHDGTCVLDKAGSYKCACLAGYTGQRCENLLEERNCSDPGGPVNGYQKITGGPGLI
                                                                                                                                                                   YVEVRDGDNRDGQIIKRVCGNERPAPIQSIGSSLHVLFHSDGSKNFDGFHAIYEEITACS
                                                                                                                                                                                                                                                                                           VVGYTIPCCRNEENECDSCLIHPGCTIFENCKSCRNGSWGGTLDDFYVKGFYCAECRAGW
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APPLICANT: WILLIAMS, P. MICKEY
APPLICANT: WOOD, WILLIAMS P. MICKEY
APPLICANT: WOOD, WILLIAMS P. MICKEY
APPLICANT: Zhang, Zemin

TITLE OF INVENTION: Secreted and Transmembrane Pol
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C37

CURRENT APPLICATION NUMBER: US/09/997,349

CURRENT FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: 60/049787

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PRIOR APPLICATION NUMBER: 60/06531

PRIOR APPLICATION NUMBER: 60/06590

PRIOR APPLICATION NUMBER: 60/06770

PRIOR APPLICATION NUMBER: 60/079910

PRIOR FILING DATE: 1998-03-20

PRIOR FILING DATE: 1998-03-20

PRIOR FILING DATE: 1998-03-20

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APPLICANT: Baker,Kevin P.
APPLICANT: Botstein,David
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Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
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Kljavin, Ivar J.
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Grimaldi, J. Christopher
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Gerritsen, Mary E
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: 1998-07-02 NUMBER: 60/091 : 1998-07-02	NUMBER: 60 : 1998-07-0	NUMBER: 60/091: 1998-07-02	NUMBER: 60: 1998-07-0	NUMBER: 60	NUMBER: 6	NUMBER: 60/0906: 1998-06-25	: 1998-06-	: 1998-06-25	: 1998-06-25 NUMBER: 60/0906	NUMBER: 60	NUMBER: 6	: 1998-06-25	: 1998-06-24	NUMBER	NUMBER: 60	56 T AWON	: 1998-06-24	: 1998-06 NUMBER:	NUMBER: 6	NUMBER: 6	8661 BEWIN	1998-06-24	1998-06	NUMBER:	NUMBER: 60	: 1998-06	1998-06-23	NUMBER: 60	NUMBER: 60	NUMBER: 6	1998-06-22	1998-	NUMBER: 60	NUMBER:	1998-06-19	1998-06-18	NUMBER: 60	NUMBER: 60/08990	1998-06-18	NUMBER	1000-06-

PRIOR

DR APPLICATION NUMBER: 60/084600
DR FILING DATE: 1998-05-07
DR FILING DATE: 1998-05-28
PR APPLICATION NUMBER: 60/087609
DR APPLICATION NUMBER: 60/087609
DR APPLICATION NUMBER: 60/087609
DR FILING DATE: 1998-06-02
DR APPLICATION NUMBER: 60/087759
DR FILING DATE: 1998-06-02
DR APPLICATION NUMBER: 60/08021
DR FILING DATE: 1998-06-04
DR APPLICATION NUMBER: 60/08025
DR FILING DATE: 1998-06-04
DR APPLICATION NUMBER: 60/08026
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DR APPLICATION NUMBER: 60/08031
DR FILING DATE: 1998-06-05
DR APPLICATION NUMBER: 60/080326
DR APPLICATION NUMBER: 60/080821
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Sequence 231, Application US/09997653
Patent No. 7034122
GENERAL INFORMATION:
APPLICANT: Ashkenazi.Avi J.
APPLICANT: Baker.Kevin P.
APPLICANT: Botstein,David
APPLICANT: Botstein,David
APPLICANT: Desmoyers,Luc
APPLICANT: Eaton,Dan L.
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DR FILING DATE: 1998-07-07
DR APPLICATION NUMBER: 60/091982
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DR APPLICATION NUMBER: 60/092182
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        Ferrara, Napoleone
Fong, Sherman
Gerber, Hanspeter
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CURRENT APPLICATION NUMBER: US/09/997,653

CURRENT FILING DATE: 2001-11-15

PRIOR APPLICATION NUMBER: 60/06787

PRIOR APPLICATION NUMBER: 60/06250

PRIOR FILING DATE: 1997-10-17

PRIOR APPLICATION NUMBER: 60/065186

PRIOR FILING DATE: 1997-11-12

PRIOR PILING DATE: 1997-11-13

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OR APPLICATION NUMBER: 60/088025
OR FILING DATE: 1998-06-04
OR APPLICATION NUMBER: 60/088026
OR FILING DATE: 1998-06-04
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OR APPLICATION NUMBER: 60/088212
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DR APPLICATION NUMBER: 60/087607

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OR APPLICATION NUMBER: 60/091360
OR FILING DATE: 1998-07-01
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OR APPLICATION NUMBER: 60/091519
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PMQVQSRETPLHQLYSAAFSKQKLQSAPTKKPALPFGDLPMGYQHLHTQLQYECISPFYR
                                      NGRHAKIGTVVSFFCNNSYVLSGNEKRTCQQNGEWSGKQPICIKACREPKISDLVRRRVL
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APPLICATION NUMBER: 60/088861 FILING DATE: 1998-06-11 APPLICATION NUMBER: 60/088876 FILING DATE: 1998-06-11 APPLICATION NUMBER: 60/089105

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REPERENCE: P27 REPERENCE: P27 REPERENCE: P27 REPERENCE: P27 REPERENCE: P27 REPLICATION N FILING DATE REPLICATION N FILING DATE REPLICATION N FILING DATE APPLICATION N	RESULT 11 US-09-989-293A-231 Sequence 231, Application US/09989293A Patent No. 7034136 GENERAL INFORMATION: APPLICANT: Bakker, Kevin P. APPLICANT: Bakker, Kevin P. APPLICANT: Baker, Kevin P. APPLICANT: Baker, Mayoleone APPLICANT: Berrara, Mapoleone APPLICANT: Fong, Sherman APPLICANT: Gerrara, Mary E. APPLICANT: Gerrara, Mary E. APPLICANT: Godowski, Paul J. APPLICANT: Godowski, Paul J. APPLICANT: Godowski, Paul J. APPLICANT: Girmaldi, J. Christopher APPLICANT: Grimaldi, J. Christopher APPLICANT: Grimaldi, J. Christopher APPLICANT: Mapier, Mary A. APPLICANT: Napier, Mary A. APPLICANT: Panni, Nicholas F. APPLICANT: Roy, Margaret Ann APPLICANT: Roy, Margaret Ann APPLICANT: Watanabe, Colin K. APPLICANT: Watanabe, Colin K. APPLICANT: Whiliams, P. Mickey APPLICANT: Walliams, P. Mickey APPLICANT: Walliams, P. Mickey APPLICANT: Walliams, P. Applicant APPLICANT: Walliams, P. Applicant APPLICANT: Walliams, P. Applicant APPLICANT: Shang, Zemin TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic	Db 361 PMQVQSRETPLHQLYSAAFSKQKLQSAFTKKPALPFGDLPMGYQHLHTQLQYECISFFYR 420 Qy 421 RLGSSRRTCLRTGKWSGRAPSCIPICGKIENITAPKTQGLRWPMQAAIYRRTSGVHDGSL 480
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              CTAETGGTAAVSFPGRASPEPRWHLMGLVSWSYDKTCSHRLSTAFTKVLPFKDWIERNMK
                                                                                                            LQISAIILHPNYDPILLDADIAILKLLDKARISTRVQPICLAASRDLSTSFQESHITVAG
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RESULT 12 US-10-067-422-9

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; Sequence 9, Application US/10067422; Patent No. 6743613; GENERAL INFORMATION: APPLICANT: Ni et al.
; APPLICANT: Ni et al.
; TITLE OF INVENTION: Bone Morphogenic Proteir; TITLE OF INVENTION: Antibodies; FILE REFERENCE: PT004P1; CURRENT APPLICATION NUMBER: US/10/067,422; CURRENT FILING DATE: 2002-02-07; PRIOR APPLICATION NUMBER: 09/685,899

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PRIOR APPLICATION NUMBER: 60/147,020
PRIOR FILING DATE: 1999-08-03
PRIOR APPLICATION NUMBER: 60/131,672
PRIOR FILING DATE: 1999-04-29
PRIOR FILING DATE: 1999-04-23
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                                                                               Sequence 4, Application Patent No. 6849426 GENERAL INFORMATION:
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Best Local Similarity
Matches 552; Conserv
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ORGANISM: Homo
-10-067-422-9
APPLICANT: Chen, Lin
APPLICANT: Pepe, Michael
TITLE OF INVENTION: Methods and Reagents
FILE REFERENCE: 02877.00008
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PRIOR FILING DATE: 1999-09-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: PCT/US00/09028 FILING DATE: 2000-04-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 2000-10-11
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96.8%;
                                                                                                                      US/10183992
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Pred. No. 8.4e-237;
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                       for Detecting
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CURRENT FILING DATE: 2002-06-28
PRIOR APPLICATION NUMBER: US 60/310,125
PRIOR FILING DATE: 2001-06-28
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
LENGTH: 1019
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   VSWSYDKTCSH-RLSTAFTKVLPFKDWIER
                                   TCEEGYKEADLPITVTENMFCAGYK-KGRYDACSGDSGG--PLVFADDSRTERRWVLEGI
                                                                                                                                                    RVQPICLAASRDLSTSFQESHI-----TVAGWNVLADVRSPGFKNDTLRSGVVSVVDSL
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                                                                         LCEEOHEDHGIPVSVTDNMFCASWEFTAPSDICTAETGGIAAVSFPGRASPEPRWHLMGL
                                                                                                                RVOPICLPT--DITT---REHLKEGTLAVVTGWG----LNENNTYSEMIQQAVLPVVAAS
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; Patent No. 5716834
; GENERAL INFORMATION:
APPLICANT: Ding, Jeak
APPLICANT: Ho, Bow
TITLE OF INVENTION: S
TITLE OF INVENTION: S
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Best Local Similarity
Matches 222; Conserv
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy
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TELEFAX: 248345
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REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 178
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T: 8110 Gatehouse Road, Suite 500 East
Falls Church
                                                                                                                                                             APKGQILLES----YPLNAHCEWTIHA----KPGFVI----
                 RPAPIQS--IGSSLHVLFHSDG-SKNFDGFH----
                                                                                                                                                                                                                                                                                                                                                                                 PGAEWNIMCRECCEYDQIECVCPGKRE-----VVGYTIPCCRNEENECDSCLIH 82
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                                                 KSEELKSLARSFRFDYVRSSTAGKSGCPDGWFEVDENCVYVTSKQRAWERAQGVCTNMAA
                                                                                                                         CPAGCSLTAGTVWGTAIYHELSSVCRAAIHAGKLPNSGGAVHVVNNGPYSDFLGSDLNGI 409
                                                                                                                                                                                               VTYTCSGNYFLMGFDTLKCNPDGSWSGSQPSCVKVADREVDCDSKAVDFLDDVGEPVRIH 349
                                                                                                                                                                                                                                     -----DDFYVKGFYCAECR--AGWYGG--DCMR-----
                                                                                                                                                                                                                                                                     PYYLIGQETLTCQGNGQWNGQIPQCKNLVFCPDLDPVNHAEHKVKIGVEQKYGQFPQGTE 289
                                                                                                                                                                                                                                                                                                                                               PNGQWSNFPPKCIR----ECAMVSSPEHGKVNALSGDMIEGATL-----RFSCDS----
                                                                                         ---QLRFVMLSLEFDYM-----
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ilarity .25.4%;
Conservative 11
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                                                                                                                                                                                                                                                                                                                                                                                                                   Score 665; DB 1;
Pred. No. 1.9e-46;
8; Mismatches 304
                                                                                     -CQYDYVEVRD-----GDNRDGQIIKRVCGN--E
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US-08-596-405-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4, Application Patent No. 5858706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Ding, Jeal APPLICANT: Ho, Bow TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: 1 NUMBER OF SEQUENCES:
                            ATTORNEY/AGENT INFORMATION:
NAME: MUTPHY, Jr., Gerald M.
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 1781-105P
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                              SOFTWARE: PatentIn Rel-
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                              STREET: 8110 Gatehouse Road, Suite 500 East CITY: Falls Church STATE: Vivilia
                                                                                                                       APPLICATION NUMBER: FILING DATE: CLASSIFICATION: 435
                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                          ZIP:
                                                                                                                                                                                                                                                                                                       COUNTRY:
               TELEPHONE:
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Bow
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                 (703)
205-8050
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INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1019 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 16.9%; Score 665; DB 1; Length 1019; Best Local Similarity 25.4%; Pred. No. 1.9e-46; Matches 222; Conservative 118; Mismatches 304; Indels 23
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                                                                                          -----KTQGLRWPWQAAIYRRTSGVHDGSLHKGAWFLVCSGALVNERTVVVAAHCVTDLG 510
LEGIVSWGSPSGCGKANQYGGFTKVNVFLSWIRQ 1017
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Search completed: April 4, 2007, 21:57:08 Job time : 50 secs

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Result
No.
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Maximum Match 100%
Listing first 1500 summaries
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Perfect score:
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Maximum DB seq length: 2000000000
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Tamm-Horsfall protends of 1,4-beta-xyla integrin beta-3 had glutamine-fructose probable transketo hypothetical prote retinovin - chicke hypothetical prote kinase-related transportein KOJHI.5 [i hypothetical prote chitinase (EC 3.2. chitinase

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	3.4.					76	1487	
	probable DEAD box					76	1485	
	al prot					76	1484	
	probable RNA-direc					76	1483	
	metalloproteinase					76	1481	
	2-aminobenzoate-Co					76	1480	
	purH bifunctional					76	1479	
	probable ADA-like					76	1477	
	oxidoreductase - D					76	1476	
	hypothetical prote					76	1475	
	membrane-associate					76	1473	
	transcription fact					76	1472	
	hypothetical prote					76	1471	
	paired box transcr					76	1470	
	rRNA methylase, YS					76	1468	
	hypothetical prote					76	1467	
	teratocarcinoma-de					76	1466	
	sperm motility inh					76	1465	
	herc2 protein - mo					76.5	1464	
	hypothetical prote					76.5	1462	
	x protein					76.5	1461	
	Xin protein - chic					76.5	1460	
	alpha tectorin - m					76.5	1458	
	protein CTRP - mal					76.5	1457	
	Munc13-2 - rat					76.5	1456	
	vitellogenin vit-6					76.5 5.5	1454	
	acetyl-CoA carboxy					76.5	1453	
	aldehyde oxidase (be					76.5	1452	
	DNA polymerase III					76.5 5	1450	
	suppressor protein					76.5	1449	
	hypothetical prote					76.5	1448	
	hymothetical prote					76.5	1447	
	protein-tyrosine k					76.5	1445	
	mucin-like peptide					76.5	1444	
	nypornericai prote integrin beta 2 ch					76.5	1443	
	finger protein - m				•	76.5 76.5	1441	
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	Ig epsilon chain C	EHMS				76.5	4	
	hynothetical prote					76.5	4 4	
	cal prot	E8326			•	76.5	4, 4	
	probable histidino	T3605				76.5	4	
	nypothetical prote					76.5	1421	
	chitinase (EC 3.2.	S3734				76.5	4.	
	hypothetical prote	E8626		30		76.5	1419	
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рь 2у	Query M Best Lo Matches Qy	A;Accession A;Accession A;Roclecule A;Residues A;Cross-ref A;Experimen C;Genetics A;Note: DXF	R;Ansorge, submitted	RESULT T08805 hypothe C;Speci C;Date:		1496 1497 1498 1499 1500	1490 1491 1492 1493 1494
1 SLR 600 GWN 61 GWN	atch cal s 180	A;Accession: T08805 A;Accession: T08805 A;Molecule type: mRNA A;Residues: 1-181 <ans; a;cross-references:="" a;experimental="" a;note:="" adult="" c;genetics:="" dkfzp586h2123.1<="" source:="" td="" uniprot:q9y432;="" uterus;=""><td>R;Ansorge, W.; Wirkner, U.; Mewes submitted to the Protein Sequence A.Reference number: 716472</td><td>RESULT 1 TO8805 TO8805 hypothetical protein DKFZp586H2123.1 C;Species: Homo sapiens (man) C;Species: 11.Jun-1999 #sequence_revisi C;Date: 11.Jun-1999 #sequence_revisi</td><td>•</td><td>76 76 76 76</td><td>7 7 7 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8</td></ans;>	R;Ansorge, W.; Wirkner, U.; Mewes submitted to the Protein Sequence A.Reference number: 716472	RESULT 1 TO8805 TO8805 hypothetical protein DKFZp586H2123.1 C;Species: Homo sapiens (man) C;Species: 11.Jun-1999 #sequence_revisi C;Date: 11.Jun-1999 #sequence_revisi	•	76 76 76 76	7 7 7 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8
ISAIII VLADVR 	larity Conser	mRNA <ans> s: UNI urce: 2123.1</ans>	rkner, Protei	ein DK apiens 99 #se		2222	
HPNYDE	24.1%; larity 99.4%; Conservative []ISAIILHPNYDPILL	PROT: Cadult	er, U.; Mewes, tein Sequence	. DKFZp5861 ens (man) #sequence		1084 1097 1206 1245 1385	908 925 926 934 967
	24.1%; 99.4%; ive ive YDPILL;	19Y4 ute	lewe	H21		21222	22772
DADIAILKLLDKARISTRVQ	Score 949; DB 2; Pred. No. 6.8e-57; 1; Mismatches 0 DADIAILKLLDKARISTRVQ	32; UNIPARC:UPI0000070151; rus; clone DKFzp586H2123	s, H.W.; Gassenhuber, e Database, May 1999	- human (fragi on 11-Jun-1999	ALIGNMENTS	T18292 S17308 T18557 VHWVB2 S34230	T27117 T37475 OPPGIT A34372 T48210 AG1979
SLRISAIILHPNYDDILLDADIAILKLLDXARISTRVQPICLAASRDLSTSFQESHITVA 60 SLRISAIILHPNYDDILLDADIAILKLLDXARISTRVQPICLAASRDLSTSFQESHITVA 60 GMNYLADVRSPGFKNDTLRSGVVSVVDSLLCEEQHEDHGIPVSVTDNMFCASWEPTAPSD 659	24.1%; Score 949; DB 2; Length 181; imilarity 99.4%; Pred. No. 6.8e-57; ; Conservative 1; Mismatches 0; Gaps 0; SLOISAIILHPNYDPILLDADIAIIKLLDKARISTRVQPICLAASRDLSTSFQESHITVA 599	770151; EMBL:AL050214 12123	J.; Wiemann, S.	ment) #text_change 09-Jul-2004		nicotinamide nucle leukemia inhibitor probable hydrogena structural polypro 156K protein - Pla	

RESULT 2 A38738

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720 K 720 | 181 K 181

coagulation factor C precursor - horseshoe crab (Tachypleus tridentatus)

N.Alternate names: coagulation-complement factor C; Limulus factor C

N;Contains: coagulation factor C heavy chain; coagulation factor C light chain peptide .

C.Species: Tachypleus tridentatus

C;Date: 04-Oct-1991 #sequence_revision 04-Oct-1991 #text_change 09-Jul-2004

C;Accession: A38738; B38738; S00105

R;Muta, T.; Misurat, Y.; Tokunaga, F.; Nakamura, T.; Toh, Y.; Ikehara, Y.; I.

J. Biol. Chem. 266, 6554-6561, 1991

A;Mital: Limulus factor C. An endotoxin-sensitive serine protease zymogen with a mosaic A;Accession: A38738; MUID:91177916; PMID:2007602

A;Accession: A38738

A;Molecule type: mRNA
A;Accession: S88738

A;Molecule type: mRNA
A;Accession: B38738

A;Molecule type: mRNA
A;Accession: B38738 A;Residues: 1-466,616,'DN',619-620,'A',622 <MU2>

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A;Molecule type: protein
A;Rolecule type: protein
A;Rolecule type: protein
A;Residues: 'S'.27-39,'S'.41,'T'.43-54,'E';691-782;950-977 <TOK>
A;Residues: 'S'.27-39,'S'.41,'T'.43-54,'E';691-782;950-977 <TOK>
A;Rosidues: 'S'.27-39,'S'.41,'T'.43-54,'E';691-81,'S'.41,'T'.43-54,'E';691-81,'S'.41,'T'.43-54,'E';691-81,'S'.41,'T'.43-54,'E';691-782,'E';691-782,'E';691-782,'E';691-782,'E';691-782,'E';691-782,'E';691-782,'E';691-782,'E';691-782,'E';691-782,'E';691-782,'E';691-782,'E';691-782,'E';691-782,'E';691-782,'E';691-782,'E';691-782,'E';691-782,'E';691-782,'E';691-782,'E';691-782,'E';691-782,'E';691-782,'E';691-782,'E';691-782,'E';691-782,'E';691-782,'E';691-782,'E';691-782,'E';691-782,'E';691-782,'E';691-782,'E';691-782,'E';691-782,'E';691-782,'E';691-782,'E';691-782,'E';691-782,'E';691-782,'E';691-782,'E';691-782,'E';691-782,'E';691-782,'E';691-782,'E';691-782,'E';691-782,'E';691-782,'E';691-782,'E';691-782,'E';691-782,'E';691-782,'E';691-782,'E';691-782,'E';691-782,'E';691-782,'E';691-782,'E';691-782,'E';691-782,'E';691-782,'E';691-782,'E';691-782,'E';691-782,'E';691-782,'E';691-782,'E';691-782,'E';691-782,'E';691-782,'E';691-782,'E';691-782,'E';691-782,'E';691-782,'E';691-782,'E';691-782,'E';691-782,'E';691-782,'E';691-782,'E';691-782,'E';691-782,'E';691-782,'E';691-782,'E';691-782,'E';691-782,'E';691-782,'E';691-782,'E';691-782,'E';691-782,'E';691-782,'E';691-782,'E';691-782,'E';691-782,'E';691-782,'E';691-782,'E';691-782,'E';691-782,'E';691-782,'E';691-782,'E';691-782,'E';691-782,'E';691-782,'E';691-782,'E';691-782,'E';691-782,'E';691-782,'E';691-782,'E';691-782,'E';691-782,'E';691-782,'E';691-782,'E';691-782,'E';691-782,'E';691-782,'E';691-782,'E';691-782,'E';691-782,'E';691-782,'E';691-782,'
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R;Tokunaga, F; Miyata, T; Nakamura, T; Morita, T; Kuma, K.
Eur. J. Biochem. 167, 405-416, 1987
A;Title: Lipopolysaccharide-sensitive serine-protease zymogen
is a novel type of serine protease.
1. a novel type of serine protease.
A;Reference number: S00105; MUID:88004461; PMID:3308457
A;Accession: S00105
A;Molecule type: protein
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;523,534,624,912/Binding site: carbohydrate (Asn) (covalent) #status predicted
;767/Binding site: carbohydrate (Asn) (covalent) #status experimental
;809,865,966/Active site: His, Asp, Ser #status predicted
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                                                                                                                                                                                                                                                               RRRVLPMQVQSRETPLHQLYSAAFSKQKLQ---SAPTKKPALPFGD-------LP
                                                                                                                                                                                                                                                                                                                    --IDGFYA--GSSIRYSCEVLHYLSGTETVTCTTNGTWSAPKPRCIKVITCONPPVPSYG
                                                                                                                                                                                                                                                                                                                                                                          GLINGRHAKIGTVVSFFCNNSYVLSGNEKRTCQQNGEWSGKQPICIK--ACREPKISDLV
                                                                                                                                                                                                                                                                                                                                                                                                                                     NETNCVYLDIRDQLQPVWKTKSCFQPSSFACMMDLSDRNKAKCDDPGPLENGHATLHGQS
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-KTQGLRWPWQAAIYRRTSGVHDGSLHKGAWFLVCSGALVNERTVVVAAHCVTDLGKVTM
                                                                                                                                              MGYQHLHTQLQYECISPFYRRLGSSRRTCLRTGKWSGRAPSCIPICGKIENITAP-----
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                                                                                         EGHYRVGSRAIYTCESRYYELLGSQGRRCDSNGNWSGRPASCIPVCGRSDSPRSPFIWNG
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Pred. No. 2e-37;
7; Mismatches 3
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N, Alternate
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C;Superfamily: complement-activating serine proteases Clr/Cls/MASP; Clr/Cls repeat C;Keywords: beta-hydroxyasparagine; complement pathway; duplication; glycoprotein; F;1-17/Domain: signal sequence #status predicted <SIG>
F;18-448,449-699/Product: Ra-reactive factor #status predicted <MAT>
F;19-135/Domain: Clr/Cls repeat homology <CIRl>
F;19-135/Domain: Clr/Cls repeat homology <CIRl>
F;143-181/Domain: Clr/Cls repeat homology <CIR2>
F;185-294/Domain: Clr/Cls repeat homology <CIR2>
F;367-432/Domain: complement factor H repeat homology <FH1>
F;367-432/Domain: complement factor H repeat homology <FH2>
F;449-691/Domain: trypsin homology <TRY>
F;449-691/Domain: trypsin homology <TRY>
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I54763
Ra-reactive
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A;Residues: 1-234,'E',236-284,'G',286-498,'K',500-542,'K',544-642,'S',644-699 <TAK>
A;Crose-references: UNIPARC:UPI000016AF63; DDBU:D17525; NID:g439712; PIDN:BAA04477.1;
A;Experimental source: liver
C;Comment: This is a serum bactericidal factor that activates complement C4 and C2 cor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: UNIPROT:P48740; UNIPARC:UPI000016AD0B; GB:I
R;Takada, F; Takayama, Y.; Hatsuse, H.; Kawakami, M.
Biochem. Biophys. Res. Commun. 196, 1003-1009, 1993
A;Title: A new member of the Cls family of complement proteins
A;Reference number: JN0883; MUID:94059062; PMID:8240317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Sato, T.; Endo, Y.; Matsushita, M.; Fujita, T.
Int. Immunol. 6, 665-669, 1994
A;Title: Molecular characterization of a novel serine protease
A;Reference number: I54763; MUID:94289349; PMID:8018603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Accession: I5470
R; Sato, T.; Endo,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Gene: GDB:MASP1; GDB:CRARF; CRARF1; PRSS5; MASP
A;Cross-references: GDB:361104; GDB:330954; OMIM:600521
                                                                                                                                                                                            F;49,178,407/Binding site: carbohydrate (ABN) (covalent) #Btatus predicted F;73-91,43-157,153-166,168-181,185-212,242-260,301-349,329-362,367-414,397-432,F;73-91,143-157,153-166,168-181,185-212,242-260,301-349,329-362,367-414,397-432,F;159/Modified site: erythro-beta-hydroxyasparagine (ABN) #Btatus predicted F;448-449/Cleavage site: Arg-Ile (autolytic) #Btatus predicted
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                                                                                  Similarity
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CRNEENECDSCLIHPGCTIFENCKSCRNGSWGGTLDDFYVKGFYCAECRAGWY----GGD
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                                                     Score 482; DB
Pred. No. 8.2e
93; Mismatches
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Biochem. J. 240, 783-787, 1986
A; Title: Cloning and sequencing of full-length cDNA encoding A; Reference number: A29768; MUID:87156625; PMID:3030286
                                                                                                                                                                                                                                                                                                                                               Biochemistry 25, 4855-4863, 1986
A;Title: Nucleotide sequence of the cDNA coding for human complement
A;Reference number: A24170; MUID:87026566; PMID:3021205
A;Accession: A24170
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                                                                                   R; Arlaud, G.J.; Willis, A.C.; Gagnon, Biochem. J. 241, 711-720, 1987
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                                                                                                                                                                                                                                                                                                                                                                                             Species: Homo sapiens (man)
;Species: Homo sapiens (man)
;Date: 15-Nov-1984 #sequence_revision 30-Jun-1991 #text change 09-Jul-2004
;Accession: A24170; A29768; A29769; S02422; A00916; A37820; S68830
;Leyrus, S.P.; Kurachi, K.; Sakariassen, K.S.; Davie, E.W.
iochemistry 25, 4855-4863, 1986
                         ;Title: Complete amino acid sequence of the A chain of ;Reference number: A29769; MUID:87241248; PMID:3036070;Accession: A29769
                                                                                                                                           ;Molecule type: mRNA
;Residues: 1-151,'L',153-705 <JOU>
                                                                                                                                                                                     Accession: A29768;
                                                                                                                                                                                                                                                                               Cross-references: UNIPROT: P00736;
                                                                                                                                                                                                                                                                                                      Residues: 1-705 <LEY>
                                                                                                                    Cross-references: UNIPARC:UPI0000001C2B; GB:X04701; NID:g29538;
                                                                                                                                                                                                                                                                  Journet, A.; Tosi, M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     subcomponent Clr (EC 3.4.21.41) precursor [validated]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Arlaud, G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Note: 152-Leu was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Residues:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Residues: 152-186 <AR3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cross-references:
                                                                                                                                                            Query Match
                                                                                                                                                                                                    502,557,654/Active
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 activate C2 and C4.
                                                                                                                                       Local
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                                                                                                                                       Similarity
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F;297-463/Product: C1r gamma fragment #status experimental <GFR>
F;309-371/Domain: complement factor H repeat homology <FH1>
F;309-371/Domain: complement factor H repeat homology <FH2>
F;376-447/Domain: complement factor H repeat homology <FH2>
F;464-705/Product: complement C1r chain B #status experimental <BCH>
F;464-97/Domain: trypsin homology <TRY>
F;71-89,146-165,161-174,176-189,193-220,250-268,309-358,338-371,376-429,406-447,451-577,
F;712-89,146-165,161-174,176-189,193-220,250-268,309-358,338-371,376-429,406-447,451-577,
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C;Superfamily: complement-activating serine proteases Clr/Cls/MASP; Clr/Cls repeat homol C;Superfamily: complement pathway; ducing serine; calcium binding; complement pathway; ducing serine protected complement pa
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A;Residues: 18-26;'L',153-160;'XX',252-255 <THI>
A;Residues: 18-26;'L',153-160;'XX',252-255 <THI>
A;Cross-references: UNIPARC:UPI0000172BC7; UNIPARC:UPI0000172BC8; UNIPARC:UPI0000172BC9
R;Pelloux, S.; Thielens, N.M.; Hudry-Clergeon, G.; Petillot, Y.; Filhol, O.; Arlaud, G.
FEBS Lett. 386, 15-20, 1996
A;Title: Identification of a cryptic protein kinase CK2 phosphorylation site in human or A;Reference number: $68830; MUID:96221263; PMID:8635594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          F;167/Modified site: erythro-beta-hydroxyasparagine (Asn) \#status experimentai F;206/Binding site: phosphate (Ser) (covalent) (by casein kinase II) \#status \#F;463-464/Cleavage site: Arg-Ile (autolytic) \#status experimental
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A;Residues: 133-137;187-211;610-613 <PEL>
A;Cross-references: UNIPARC:UPI0000172BCA; UNIPARC:UPI0000172BCB; UNIPARC:UPI0000172BCC
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A;Residues: 464-705 AR2>
A;Cross-references: UNIPARC:UPI000015033B
A;Cross-references: UNIPARC:UPI000015033B
A;Trielens, N.M.; Aude, C.A.; Lacroix, M.B.; Gagnon, J.;
J. Biol. Chem. 265, 14469-14475, 1990
A;Title: Ca(2+) binding properties and Ca(2+)-dependent
A;Reference number: A37820; MUID:90354439; PMID:2387866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEBS' Lett. 222, 129-134, 1987
A; Title: Identification of erythro-beta-hydroxyasparagine A; Reference number: S02422; MUID:88005128; PMID:2820791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               F;1-17/Domain: signal sequence #status predicted <SIG>
F;17-138/Domain: C1r/C1s repeat homology <C1R1>
F;18-463/Product: complement C1r chain A #status experimental <ACH>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Arlaud, G.J.; Gagnon, J.
Biochemistry 22, 1758-1764, 1983
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F;193-302/Domain: Clr/Cls repeat homology <ClR2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GDB:119729; OMIM:216950
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A;Note: 152-Leu was also found
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erences: UNIPARC:UPI0000172BC5
EGCFYDYVKISADKKSLGRFCGQLGSPLGNPPGKKEFMSQGNKMLLTFHTDFSNEEN--G
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                                                                                                            ---VC-------PGKREVVGYTIPCC--
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Pred. No. 1.6e-19;
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A;Note: parts of this sequence, including the company of the compa
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A;Residues: 1-686 <JEN>
A;Cross-references: UNIPARC:
A;Experimental source: tissue liver
A;Note: submitted to GenBank, December 1996
A;Note: parts of this sequence, including the sequence of the seque
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Title: A second serine protease associated with mannan-binding A;Reference number: A59271; MUID:97242412; PMID:9087411 A;Accession: A59271 Ai,Status: nucleic acid sequence not shown; not compared with concessions.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R; Thiel, S.; Vorup-Jensen, T.;
Nature 386, 506-510, 1997
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;Thiel, S.; Vorup-
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complement pathway; duplication; hydrolase; serine |
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F;1-15/Domain: signal sequence #status predicted <SIG>
F;16-444,445-686/Product: Ra-reactive factor 2 #status predicted <MAT>
F;19-134/Domain: Clr/Cls repeat homology <CIR1>
F;142-180/Domain: EGF homology <EGF>
F;144-293/Domain: Clr/Cls repeat homology <CIR2>
F;300-361/Domain: complement factor H repeat homology <FH1>
F;366-430/Domain: complement factor H repeat homology <FH2>
F;445-679/Domain: trypsin homology <TRY>
F;445-679/Domain: trypsin homology <TRY>
F;772-90,142-156,152-165,167-180,184-211,241-259,300-348,328-361,366-412,396-430,434-552,F;158/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted
F;444-445/Cleavage site: Arg-Ile (autolytic) #status predicted
F;483,532,633/Active site: His, Asp, Ser #status predicted
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                                                                                                                                                                                                                                                     AHCVTDLGKVTMIKTADLKVVLGKFYRDDDRDEKTIQSLQ-----ISAIILHPNY-DP
                                                                                                                                                                                                                                                                                                                                                                                                                                         DRPMPACSIVDCGPP--DDLPSGRV---------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SGKQPIC-IKACREPKISDLVRRRVLPMQVQSRETPLHQLYSAAFSKQKLQSAPTKKPAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DFLKIQTDREEHGPFCGKTLPHRIETKSNTVTITFVTDESGDHTGWKIHYTSTAHACPYP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FDGFHAIY--EEITACSSSP-----CFHDGTCVLDKAGSYKCACLAGYTGQR----CENL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LCEYDFVKLSSG----AKVLATLCGQESTDTERAPGKDTFYSLGSSLDITFRSDYSNEKP
                                                                                                      DTLRSGVVSVVDSLLCEEQHEDHGIP-VSVTDNMFCASWEPTAPSDICTAETGGIAAVSF
                                                                                                                                                                               ILLDADIAILKLLDKARISTRVQPICLAASRDLSTSFQESHITVAGWNVLADVRSPGFKN
                                                                                                                                                                                                                   AHAVYE----QKHDASALDIRMG-----TLKRLSPHYTQAWSEAVFIHEGYTHD
                                                                                                                                                                                                                                                                                         SARTTGGRIYĞGQKAKPGDFPWQVLILGGTT
                                                                                                                                                                                                                                                                                                                                                                                                   PFGDLPMGYQHLHTQLQYECISPFY-RRLGSSRRTCLRTGKWSG-----RAPSCIPICGK
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                    PGRASPEPRWHLMGLVSWSYDKTCSHRLSTAFTKVLPFKDWIE
                                                                     RNLMYVDIPIVDHQKCTAAYEKPPYPRGSVTANMLCAGLE-SGGKDSCRGDSGG--ALVF
                                                                                                                                           AGFONDIALIKLNNKVVINSNITPICLPRKEAESFMRTDDIGTASGWG----LTQRGFLA
                                                                                                                                                                                                                                                                                                                           IENITAPKTQGLR-----WPWQAAIYRRTSGVHDGSLHKGAWFLVCSGALVNERTVVVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FTGFEAFYAAEDIDECQVAPGEAPTCDHH----CHNHLGGFYCSCRAGYVLHRNKRTCSAL
LDSETERWFYGGIVSWGSMNCGEAGQYGVYTKVINYIPWIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                               -GVTTYKAVIOYSCEETFYTMKVNDGKYVCEADGFWTSSKGEKSLPVCEPVCGL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 400.5; DB 1; Pred. No. 2.5e-19;
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A;Cross-references: UNIPROT:P15156; UNIPARC:UPI000012700B; EMBL:X16160; NID:g49621; PIDN A;Note: part of this sequence, including the amino ends of both the heavy and light chair c;Superfamily: complement-activating serine proteases C1r/C1s/MASP; C1r/C1s repeat homol C;Keywords: beta-hydroxyasparagine; calcium binding; duplication; glycoprotein; hydrolast F;1-21/Domain: signal sequence #status predicted <SIG-F;17-133/Domain: C1r/C1s repeat homology <C1R1>F;22-444/Product: serine proteinase heavy chain #status experimental <HCH>F;141-177/Domain: EGF homology <EGFP>F;181-293/Domain: C1r/C1s repeat homology <C1R2>F;191-293/Domain: C1r/C1s repeat homology <C1R2>F;191-293/Domain: complement factor H repeat homology <FH1>F;365-428/Domain: complement factor H repeat homology <FH2>F;445-682/Domain: trypsin homology <TRY>F;446-695/Product: serine proteinase light chain #status experimental <LCH>F;49-46-595/Product: serine proteinase light chain #status experimental <LCH>F;190,413/Binding site: carbohydrate (Asn) (Covalent) #status predicted F;180,413/Binding site: carbohydrate (Asn) (Covalent) #status predicted F;482,536,638/Active site: His, Asp, Ser #status predicted
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A;Title: Complete primary structure of a calcium-dependent A;Reference number: S05008; MUID:89325606; PMID:2753140
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Residues: 1-695 <KIN>
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Kinoshita, H.; Sakiyama,
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Best Local Similarity
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-Sep-1999 #sequence_revision 10-Sep-1999
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LLDKARISTRVQPICLAASRDLSTSFQESH---ITVAGW-----
                                                                                   M-IKTADLKVVLGKFYRDDDRDEKTIQSLQISAIILHPNYDP-----ILLDADIAILK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GOILL----ESYPLNAHCEWTIHAKPGFVIQLRFVMLSLEFDYMCQYDYVEVRDGDNRDG
                                               MYVGSTSVRM-
                                                                                                                                                                                GLRWPWQAAIYRRTSGVHDGSLHKGAW----
                                                                                                                                                                                                                                                                        TQLQYECISPFY----RRLGSSRRTCLRTGKWSG-----RAPSCIPICGKIENITAPKTQ
                                                                                                                                                                                                                                                                                                                                                              EPKISDLVRRRVLPMQVQSRETPLHQLYSAAFSKQKLQSAPTKKPALPFGDLPMGYQHLH
                                                                                                                                                                                                                                                                                                                                                                                                                KDVVKISCVDGFEAVEGNVGSTFFYS-----
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                                                                                                                                   ---IQQRIFGGFPAKIQSFPWQVFFEFPRAGGALIGEHWVLTAAHVVEGNSDPS
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Pred. No. 7.6e-18;
1; Mismatches 227;
                                          ENLANVQKLTTDRVI IHPGWKPGDDLSTRTNFDNDIALVR
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                                                                                                                                                                                                                                -CAANGSWVNDELGIELPKCVPVCG
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                                                                                                                                                                                - FLVCSGALVNERTVVVAAHCVTDLGKVT
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polyprotein - African clawed frog C, Species: Xenopus laevis (African clawed frog C, Date: 22-Oct-1999 #sequence_revision 22-Oct C, Accession: T30337
R, Yang, J.C.; Lindsay, L.L.; Hedrick, J.L. submitted to the EMBL Data Library, March 199 A, Description: cDNA cloning of ovochymase, a A, Reference number: Z20829
A, Accession: T30337
A, Status: preliminary; translated from GB/EME A, Molecule type: mRNA A, Description: TSCA , VAN A, DESCRIPTION: TSCA 
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A;Cross-references: UNIPROT:Q91674; UNIPARC:UPI00000FBA76;
C;Superfamily: tryosin related nolumnotoin.
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      VVLGKFYRDDDR--DEKTIQSLQISAIILHPNYDPILLDADIAILKLLDKARISTRVQPI
                                                                                                                          AAI-YRRTSGVHDGSLHKGAWFLVCSGALVNERTVVVAAHCVTDLGKVTMIKTAD---LK
                                                                                                                                                                                         AIALDVCGMAPM
                                                                                                                                                                                                                                                  ---LQYECISPFYRRLGSSRRTCLRTGKWSGRAPSCIP-ICGKIENITAPKTQGLRWPWQ
                                                                                                                                                                                                                                                                                                           TLPLPISSPENTMLIRFKTDMENSYPG--FKVKFSFVPKEKQFSLPVDDTPT-ISMLHPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GRHAKIGTVVSFFCNNSYVLSGNEKRTCQQNGEWSGKQPICIKACREPKISDLVRR----R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DKAGSYKCACLAGYTGORCENLLEERNCSDP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KMIRKVCGSTIPSPLIVRSNKVTVTFFSDGTFTGRGFEIQFLAIPTKAASAC--GSAKIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QIIKRVCGNERPAPIQSIGSSLHVLFHSDGSKNFDGFHAIYEEITACSSSPCFHDGTCVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NGTVRYPLSGNYSINSVCRWMLAVQKAKTIEIRFLQLDIEDHATCTFDYLSFTVNE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KGQI----LLESYPLNAHCEWTIHAKPGFVIQLRFVMLSLEFDYMCQYDYVEVRDGDNRDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       G--CVSWGLGCGRSWGAKQIIRSQSGSPAIFSRVSSVLDFLRPPKLTGGCSSKGRTITGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GFYCAE----CRAGW-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CPGKREVVGY-----TIPCCRNEENECDSCLIHPGCTIFENCKSCRNGSWGGTLDDFYVK 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PVPN--VRDPKFYVAGLVSWG--KKCG--TYGIYTKVKNYKDWILQTMQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SFPGRASPEPRWHLMGLVSWSYDKTCSHRLSTAFTKVLPFKDWIERNMK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LRSGVVSVVDSL-----LCEEQHEDHGIPVSVTDNMFCASWEPTAPSDICTAETGGIAAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LKDPVKMGPTVSPICLPGT---SSEYEPSEGDLGLISGWGRTERRNIVIQLR----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   wed frog
(African clawed frog)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    101;
                                                                                                                                                                                                                                                                                                                                                                   TPLHQLYSAAFSKOKLQSAPTKKP-ALPFGDLPMGYQHLHTQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 354; Ub 4,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -MIYSPNYPDPYPRLKTCSWIIEAPENHIVKLKFEDFNVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        March 1998
hymase, a ci
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----YGGDCMRCGQVLRAP
                                                                                                                                                                                      WLPRIVEGEE -- ASPNS -- -- WPWQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       260;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -GGPVNGYQKITGGPGLIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                  ----QLIARLCGY
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                                                                  - IRAAEPSYWT
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-DHNRMLNESTEQIRNIKTIRIHDNYNSETYDNDIALLYLEEPLDLNDFVRPV

691

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C;Superfamily: complement-activating serine proteases Clr/Cls/MASP; Clr/Cls C;Keywords: differentiation; glycoprotein; hydrolase; serine proteinase F;1-21/Domain: signal sequence #status predicted <SIG> F;17-133/Domain: Clr/Cls repeat homology <ClR> F;22-694/Product: serine protease homolog #status predicted <MAT>
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C; Superfamily
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Sakai, H.; Nakashima, S.; Yoshimura, S.; Nishimura, Y.; Sakai, N.; Nozawa, Ngene 209, 87-94, 1998
Gene 209, 87-94, 1998
A;Title: Molecular cloning of a cDNA encoding a serine protease homologous to
A;Reference number: JC6554; MUID:98192519; PMID:9524231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: mRNA
A; Residues: 1-694 < SAK>
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;444-681/Domain: trypsin homology <TRY>
;180,412/Binding site: carbohydrate (Asn) (covalent)
;481,535,637/Active site: His, Asp, Ser #status predi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Accession: JC6554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Species: Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           --ELTDHMLCAGFPSSKEKDACQGDSGGPLVCQ-----NEKEQFSIYGLVSWG--EGCG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PVSVTDNMFCASWEPTAPSDICTAETGGIAAVSFPGRASPEPRWHLMGLVSWSYDKTCSH 699
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                                                                   CQQNGEWSGK---
                                                                                                                                                                                            TGQNKGWKLRYHGDPIPCPKEISANSIWEPEKAKYVFKD
                                                                                                                                                                                                                                          SKNFDGFHAIY----
                                                                                                                                                                                                                                                                               D-----VEPADSEGNCHDSLTFAAKNQQFGPYCGNGFPGPLTIKTQSNTLDIVFQTDL
                                                                                                                                                                                                                                                                                                                     DYMCQYDYVEVRDGDNR------DGQIIKRVCGNERPAP--IQSIGSSLHVLFHSDG
                                                                                                                                                                                                                                                                                                                                                              DMRTCGVNCSGDVFTALIGEIASPNYENPYPENSRCEYQIRLQEGF--RLVLTIRREDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                    FAAYYSAVDVNECTDFTDVP-CSHF----
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                            CQSNGQWSNSRLECQPV---
                                                                                                                                                  QRCENLLEERNCSDPGGPYNGYQKITGGPGLINGRHAKIGTVVSFFCNNSYVLSGNEKRT 328
                                                                                                                                                                                                                                                                                                                                                                                                        DCMR-----CGQVLRAPKGQILLES----YPLNAHCEWTIHAKPGFVIQLRFVMLSLEF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ECCEYDQIECVCPGKRE--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----NECDSCLIHPGCTIFENCKSCRNGSWGGTLDDFYVKGFYCAECRAGWYGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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EGF homology <EGF>
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                                                             QPICIKACREPKISDLVRRRVLPMQVQSRETPLHQLYSAAFSKQKL
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                                                                                                                                                                                                                                      -EEITACS-----SSPCFHDGTCVLDKAGSYKCACLAGYTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 340.5; DB 2
Pred. No. 2.7e-15;
8; Mismatches 244
                            -DCGVPE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         UNIPARC:UPI00000E6CA8; DDBJ:D88250; NID:g3080541; in glial cell differentiation and cartilage remode
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    -CNN-----FIGGYFCS-CPPEYFLH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2;
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                          -PIENGKVEDPEDTVFGSV-----
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                                                                          A;Molecule type: protein
A;Residues: 16-38;68-116;170-236;246-262;265-280;282-284;287-308,315-363;384-394;421-43
A;Residues: 16-38;68-116;170-236;246-262;20100001728CD; UNIPARC:UPI00001728CE
A;Cross-references: UNIPARC:UPI00001728D5
BD3; UNIPARC:UPI00001728D4; UNIPARC:UPI00001728D5
B7;Tosi, M.; Duponchel, C.; Meo, T.; Couture-Tosi, E.
J. Mol. Biol. 208, 709-714, 1989
A;Title: Complement genes Cir and Cis feature an intronless serine protease domain clos
A;Reference number: 805634; MUID:90040704; PMID:2553984
A; Molecule type: DNA
A; Residues: 356-513, 'G', 514-688
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                                                             A; Accession: S05634
                                         A; Status: not compared with conceptual translation
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S26732

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C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-May-2004 C;Caccession: A40496; A27381; S00224; S26732; S05634; A05140; A25396; A38407; R;Kusumoto, H.; Hirosawa, S.; Salier, J.P.; Hagen, F.S.; Kurachi, K. Proc. Natl. Acad. Sci. U.S.A. 85, 7307-7311, 1988 A;Title: Human genes for complement components C1r and C1s in a close tail-to A;Reference number: A40496; MUID:89017187; PMID:2459702
                                                                     A;Cross-references: UNIPARC:UPI0000126BF6; GB:M18767; NID:g179647; PIDN:AAA51853. R;Mackinnon, C.M.; Carter, P.E.; Smyth, S.J.; Dunbar, B.; Fothergill, J.E. Eur. J. Bicchem. 169, 547-553, 1987
A;Title: Molecular cloning of cDNA for human complement component Cls. The comple A;Reference number: S00224; MUID:88082788; PMID:3500856
A;Accession: S00224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement subcomponent C1s (EC 3.4.21.42) N;Alternate names: C1 esterase precursor C;Species: Homo sapiens (man)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT
C1HUS
                                                                                                                                                                                                                                                                             R;Tosi, M.; Duponchel, C.; Meo, T.; Julier, C.
Biochemistry 26, 8516-8524, 1987
A;Title: Complete cDNA sequence of human complement Cls
A;Reference number: A27381; MUID:88163522; PMID:2831944
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                      A; Molecule type: mRNA
A; Residues: 1-688 < MAC>
                                                                                                                                                                                                                 A; Molecule type: mRNA
A; Residues: 1-688 < TOS>
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A;Residues: 1-688 <KUS>
    A;Cross-references:
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  UNIPARC: UPI0000126BF6;
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EMBL:X06596; NID:g29542;
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    PIDN: CAA29817.1;
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A;Reference number: A38407; MUID:91175725; PMID:2007122
A;Accession: A38407
A;Accession: A38407
A;Molecule type: protein
A;Residues: 131-134,'X',136-146,'X',148-150;155,'X',157-162;166-170,'X',172-174,'X',176-17,'X',518-627,'X',529-637
A;Residues: 131-134,'X',136-146,'X',148-150;155,'X',157-162;166-170,'X',619-627,'X',629-635
A;X',387-402,'X',404-408;416-424,'X',426-431;547-556;592-597,617,'X',619-627,'X',629-635
A;Cross-references: UNIPARC:UPI0000172BEB; UNIPARC:UPI0000172BEB; UNIPARC:UPI0000172BEB; UNIPARC:UPI0000172BEB; UNIPARC:UPI000172BEB; UNIPARC:UPI000172BEB; UNIPARC:UPI0000172BEB; UNIPARC:UPI00000172BEB; UNIPARC:UPI0000172BEB; UNIPARC:UPI0000172BEB; UNIPARC:UPI0000172BEB; UNIPARC:UPI0000172BEB; UNIPARC:UPI0000172BEB; UNIPARC:UPI0000172BEB; UNIPARC:UPI000017ZBEB; UNIPARC:UPI000017ZBEB; 
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A;Rolecule type: protein
A;Residues: 16-25;%',203-207 <THI>A;Residues: 16-25;%',203-207 <THI>A;Cross-references: UNIPARC:UPI0000172BF2; UNIPARC:UPI0000172BF3
A;Cross-references: UNIPARC:UPI0000172BF2; A;Cross-references: UNIPARC:UPI0000172BF3
A;Thielens, N.M.; Van Dozaselaer, A.; Gagnon, J.; Arlaud, G.J.
Biochemistry 29, 3570-3578, 1990
A;Title: Chemical and functional characterization of a fragment of Cls con
A;Title: Chemical and functional characterization of a fragment of Cls con
A;Reference number: A32672; MUID:90283368; PMID:2141278
A;Roter annotation; erythro-beta-hydroxyasparagine site, content
A;Note: about half of the A chains contain erythro-beta-hydroxyasparagine
C;Comment: This protein is a serine proteinase that combines with Clq and s C2 and C4.
C;Comment: C1s is a dimer of identical chains, each of which is activated
C;Genetics:
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A;Residues: 16-61;168-219;287-293,'K',295-334;384-445 <SPY>
A;Cross-references: UNIPARC:UPI0000172BDE; UNIPARC:UPI0000172BDF; |
R;Hess, D, Schaller, J.; Rickli, E.E.
Biochemistry 30, 2827-2833, 1991
A;Title: Identification of the disulfide bonds of human complement
A;Reference number: A38407; MUID:91175725; PMID:2007122
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R;Carter, P.E.; Dunbar, B.; Fothergill, J.E.
Biochem, J. 215, 565-571, 1983
A;Title: The serine proteinase chain of human complement component Cls.
A;Reference number: A05140; MUID:84104122; PMID:6362661
A;Accession: A05140
A;Molecule type: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Note: the list of introns may be C;Superfamily: complement-activatin C;Keywords: acute phase, beta-hydro F;1-15/Domain: signal sequence #sta
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A;Title: Human complement
A;Reference number: A25396
A;Accession: A25396
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A;Residues: 438-483,'X',485-500;503-534;542-558;561-572,'A',574-601;617-623;626-644;647
A;Cross-references: UNIPARC:UPI0000172BD7; UNIPARC:UPI0000172BD8; UNIPARC:UPI0000172BD9
R;Spycher, S.E.; Nick, H.; Rickli, E.E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: GDB:119730; OMIM:120580
A;Map position: 12p13-12p13
A;Introns: 291/1; 329/3; 356/1; 399/1; 424/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Superfamily: complement-activating serine proteases Clr/Cls/MASP; Clr/Cls Keywords: acute phase; beta-hydroxyasparagine; calcolum binding; complement; l-15/Domain: signal sequence #status predicted <SIG>;11-127/Domain: Clr/Cls repeat homology <CIR1>;16-688/Product: complement subcomponent Cls #status experimental <MAT>;16-488/Product: complement subcomponent Cls chain A (heavy chain) #status;135-171/Domain: EGF homology <EGF>;15-287/Domain: Clr/Cls repeat homology <CIR2>;15-287/Domain: Clr/Cls repeat homology <CIR2>;15-287
                                                                                                                                                                                                                                         ;438-689/Product: complement subcomponent C1s chain B (light chain) #status experiments;438-675/Domain: trypsin homology <TRY>
;65-83,135-147,143-156,158-171,175-202,234-251,294-341,321-354,359-403,386-421,425-549,
;149/Modified site: erythro-beta-hydroxyasparagine (Asn) (partial) #status experimental;
;174,406/Binding site: carbohydrate (Asn) (covalent) #status experimental;
;433-438/Cleavage site: Arg-Ile (complement subcomponent C1r) #status experimental;
;437-438/Csavage site: Arg-Ile (complement subcomponent C1r)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;294-354/Domain: complement factor H repeat homology <FH1>;359-421/Domain: complement factor H repeat homology <FH2>;418-688/Product: complement subcomponent C1s chain B (light chain)
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                                                           Query Match
Best Local Similarity
Matches 163; Conserv
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                                                           Conservative
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                                                                                                   8.5%;
                                                           83;
                                            Score 334; DB 1;
Pred. No. 7.4e-15;
3; Mismatches 246
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C;Date: 19-May-1995 #sequence revision 09-Aug-1996 #text_change
C;Accession: A56318; B43090
R;Kitamoto, Y.; Veile, R.A.; Donis-Keller, H.; Sadler, J.E.
Biochemistry 34, 4562-4568, 1995
A;Title: cDNA sequence and chromosomal localization of human ent
A;Reference number: A56318; MUID:95234679; PMID:7718557
A;Accession: A56318
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A;Reference number: A43090; MUID:94329561; A;Accession: B43090
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VSWSYDKTCSHRLSTAFTKVLPFKDWIERNMK 720
                                                                                                                              EDHGIPVS-----VTDNMFCASWEPTAPSDICTAETGGIAAVSFPGRASPEPRWHLMGL
                                                                                                                                                                                                                                                         PICLAASRDLSTSFQESHITVAGWNVLADVRSPGFKND---TLRSGVVSVVDSLLCEEQH
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                                                               VEK--PTADAEAYVFTPNMICAGGE--KGMDSCKGDSGGAFAVQDP---NDKTKFYAAGL
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enteropeptidase (EC 3.4.21.9) precursor [validated]

09-Jul-2004

enterokinase, the proteoly

A; Molecule type: mRNA
A; Residues: 1-1019 < KKIT>
A; Cross-references: UNIPROT: P98073; UNIPARC: UPI000003FE65; GB:
R; Kitamoto, Y.; Yuan, X.; Wu, Q.; McCourt, D.W.; Sadler, J.E.
Proc. Natl. Acad. Sci. U.S.A. 91, 7588-7592, 1994
A; Title: Enterokinase, the initiator of intestinal digestion, GB:U09860; .E. NID: 9746412; PIDN

acid sequence not shown

PMID:8052624

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ed by a disulfide bond. Possibly, ducts.
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F;643-677/Domain: LDL receptor ligand-binding repeat homology <LDL2>
F;6643-677/Domain: LDL receptor ligand-binding repeat homology #status stypical
F;678-783/Domain: scavenger receptor cysteine-rich domain homology #status stypical
F;785-1019/Product: enteropeptidase light chain #status predicted <LCH>
F;785-1019/Product: trypsin homology <TRY>
F;785-1014/Domain: trypsin homology <TRY>
F;116,147,179,328,335,388,440,470,503,534,630,682,706,725,848,887,909,949/Binding si
F;772-896,810-826,910-977,941-956,967-995/Disulfide bonds: #status predicted
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A;Map position: 21q21-21q21
C;Complex: Mature enteropep
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F;342-504/Domain:
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;,Residues: 749-1019 <KI2>
;Cross-references: UNIPARC:UPI0000172B0B; GB:U09860
;,Comment: The mechanism of association with the membrane of the intestinal brush
;,Comment: The methanism of association with the heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Description: cleaves activation peptide from trypsinogen to produce s;Pathway: intestinal digestive hydrolase cascade;Superfamily: enteropeptidase; CIr/CIs repeat homology; LDL receptor;Keywords: glycoprotein; hydrolase; serine proteinase; transmembrane;1-784/Product: enteropeptidase heavy chain #status predicted <HCH>
7,2-38/Domain: transmembrane #status predicted <TMM>
7,184-221/Domain: LDL receptor ligand-binding repeat homology <LDL1>
7,342-504/Domain: MAM homology <MAM>
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Matches
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     GDSGG
                                    AETGGIAAVSFPGRASPEPRWHLMGLVSWSYDKTCSHRLSTAFTKVLPFKDWIE
                                                                                                         VLADVRSPGFKNDTLRSGVVSVVDSLLCEEQHEDHGIPVSVTDNMFCASWEPTAPSDICT
                                                                                                                                                                    ISAIILHPNYDPILLDADIAILKLLDKARISTRVQPICLAASRDLSTSFQESHITVAGWN
                                                                                                                                                                                                                                                      GAWFLVCSGALVNERTVVVAAHCVTDLGKVTMIKTADLKVVLGKFYRDDDRDEKTIQSLQ
                                                                                                                                                                                                                                                                                              QCNHKSC-----
                                                                                                                                                                                                                                                                                                                               GSSRRTCLRTGKWSGRAPSCIPICGKIENITAPKTQGLRWPWQAAIYRRTSGVHDGSLHK
                                                                                                                                                                                                                                                                                                                                                                     GSGNSSKPIFSTDGGPF--VKLNTAPD--
                                                                                                                                                                                                                                                                                                                                                                                                      QVQSRETPLHQLYSAAFSKQKLQSAPTKKPALPFGDLPMGYQHLHTQLQYECISPFYRRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RHAKIGTVVSFFCNNSYVLSGNEKRTCQQNGEWSGKQPICIKACREPKISDLVRRRVLPM 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LDKAGSYKC---ACLA-----GYTGQRCENLLEERNCSDPGGPVNGYQKITGGPGLING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RPAPIQSIGSSLH------VLFHSDGSKNF-DGFHAIYEEITACSSSPCFHDGTCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SYPNIAFCVWILNAQKGKNIQLHF----QEFDLENINDVVEIRDGEEADSLLLAVYTG--
                                                                      T---VVYQGTTANILQEADVPLLSNERCQQQMPEY----NITENMICAGYE-EGGIDSCQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   --KADHFQCKNGECVPLVNLCDGHL--HCEDGSDEADC-----VRFFNGTTNNNGLVRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -PGPVKDVFSTTNRMTVLLITNDVLARGGFKANFTTGYHLGIPE-----PC-----
                                                                                                                                             IDEIVINPHYNRRRKDNDIAMMHLEFKVNYTDYIQPICLPEENQVFPPGR--NCSIAGWG
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PLMCQENNRWFLAGVTSFGYKCALPNR-PGVYARVSRFTEWIQ
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                                                                                                                                                                                                                                                                                            -GKKLAAQDITPKI--VGGSNAKEGAWPWVVGLY----YGGR---
                                                                                                                                                                                                                                                                                                                                                                                                                                          -----HTACAENWTTQISNDVC------QLLGL
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Pred. No. 1.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ser #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1.7e-14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           225;
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                                                                                                                                                                                                                                                                                                                                                                   -GHLILTPSQQCLQDSLIRL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1019;
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C;Punction:

C;Punction: cleaves activation peptide from trypsinogen to produce active trypsin A,Description: cleaves activation peptide from trypsinogen to produce active trypsin A,Pethway: intestinal digestive hydrolase cascade

C;Superfamily: enteropeptidase; Clr/Cls repeat homology; LDL receptor ligand-binding re;

C;Keywords: glycoprotein; hydrolase; serine proteinase; transmembrane protein; zymogen F;22-38/Domain: transmembrane #status predicted <MCH>
F;22-38/Domain: tenteropeptidase mini chain #status predicted <MCH>
F;118-799/Product: enteropeptidase mini chain #status predicted <MCH>
F;118-799/Product: enteropeptidase mini chain #status predicted <HCH>
F;118-799/Product: enteropeptidase havy chain #status predicted <HCH>
F;37-519/Domain: MAM homology <MAM>
F;351-519/Domain: MAM homology <MAM>
F;551-646/Domain: Clr/Cls repeat homology <Cll>
F;658-692/Domain: LDL receptor ligand-binding repeat homology <LDL2>
F;658-692/Domain: LDL receptor ligand-binding repeat homology <LDL2>
F;658-692/Domain: scavenger receptor cysteine-rich domain homology *status atypical <SR
F;800-1034/Product: enteropeptidase light chain #status predicted <LCH>
F;116,147,170,194,283,343,350,403,455,485,518,549,645,697,701,721,740,761,804,863,902,9
F;187-911,825-841,925-992,956-971,982-1010/Disulfide bonds: #status predicted
F;840,891,986/Active site: His, Asp, Ser #status predicted
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C;Complex: Mature enteropeptidase is variously reported to contain two (heavy and lied by a disulfide bond. Possibly, conversion from membrane-bound to soluble forms in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     enteropeptidase (EC 3.4.21.9) precursor [validated] N;Alternate names: enterokinase C;Species: Sus scrofa domestica (domestic pig) C;Date: 07-Oct-1994 #sequence_revision 09-Aug-1996;C;Date: Name: Na
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Matsushima, M.; Ichinose, M.; Yahagi, N.; Kakei, N.; Tsukada, J. Biol. Chem. 269, 19976-1998, 1994
A;Tille: Structural characterization of porcine enteropeptidase A;Reference number: A53663; MUID:94327548; PMID:8051081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Residues: 1-1034 <MAT>
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                                                                                                   LHKGAWFLVCSGALVNERTVVVAAHCVTDLGKVTMIKTADLKVVLGKFYRDDDRDEKTIQ 539
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                                                                                                                                                                                                                                                                                                                            RRTCLRTGKWSGRAPSCIPICGKIENITAPKTQGLR-----WPWQAAIYRRTSGVHDGS 479
                                                                                                                                                                                                                                                                                                                                                                                                                                                 NSSMPFFSSGGGPF--VKLNTAPNGSLILTASE----
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LLCGASLVSRDWLVSAAHCV--YGR--NLEPSKWKAILG-LHMTSNLTSPQIV
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s.
S. Superfamily: coagulation factor X; EGF homology; Gla domain homology; try C; Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; F;1-33/Domain: signal sequence #status predicted <SIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein C (activated) (EC 3.4.21.69)
NyAlternate names: vitamin K-dependen
C;Species: Mus musculus (house mouse)
C;Date: 10-Sep-1999 #sequence_revisio
C;Accession: JXO210
R;Tada, N.; Sato, M.; Tsujimura, A.;
J. Biochem. 111, 491.495, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Title: Isolation and characterization of a mouse protein C cDNA. A;Reference number: JX0210; MUID:92316897; PMID:1618739 A;Accession: JX0210
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F;42-196,199-461/Product: protein C #status predicted
F;42-196/Domain: light chain #status predicted <PCL>
F;91-130/Domain: EGF homology <EG1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
A; Residues: 1-461 <TAI
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;47,48,55,57,60,61,66,67,70,76/Modified site: gamma-carboxyglutamic acid (Glu);112/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted;121-130,139-150,146-159,161-174,182-319,238-254,373-387,398-426/Disulfide bond;214,290,355/Binding site: carbohydrate (Asn) (covalent) #status predicted;214,290,402/Active site: His, Asp, Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          rotein C (activated) (EC 3.4.21.69) precursor - mouse ;Alternate names: vitamin K-dependent serine proteinase ;Species: Mus musculus (house mouse) ;Date: 10-Sep-1999 #text_change ;Date: 10-Sep-1999 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;199-461/Domain: heavy chain #status predicted <PCH>;199-211/Domain: activation peptide #status predicted <ACT>;299-211/Product: vitamin K-dependent serine proteinase #status predicted <VIT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            139-174/Domain: EGF homology <EG2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;Cross-references: UNIPROT:P33587; UNIPARC:UPI00000278D0; GB:D10445; Experimental source: liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
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197
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                                                                                                                                                                                                                                YKCACLAGYTGORCENLLEERNCSDPGGPVNGYQKITGGPGL-----INGRHAKIGTVV
                                                                                                                                                                                                                                                                                                                                                                                WGISSIPAHPDPVFSSSEHAHQVLRVRRANSFLE
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                                                                                                                                                                                                                                                                                                                              CGNERPAPI-QSIGSSLHVLFHSDGSKNFDGFHAIYEEITACSSSPCFHDGTCVLDKAGS
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                                       QSRETPLHQLYSAAFSKQKLQSAPTKKPALPFGDLPMGYQHLHTQLQYECISPFYRRLGS
                                                                                                                                   SFFCNNSYVLSGNEKR-----TCQQNGEWSGKQPICIKACREPKISDLVRRRVLPMQV
                                                                                                                                                                                   FSCSCDKGWEGKFCQQELRFQDC-----RVNNGGCLHYCLEESNGRRCA----
                                                                                                                                                                                                                                                                                 CDFEEAQEIFQNVEDTLAFWI----
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                                                                                            CAPGYELADDHMRCKSTVNFPCGKLGRWIEK-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 320; DB 1; Length 461; Pred. No. 4.2e-14; O; Mismatches 174; Indels 2
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545 AIILHPNYDPILLDADIAILKLLDKARISTRVQPICL----AASRDLSTSFQESHITVAG
                                                                                                                                                                                                                                                                                                                                                                                                                236 --LACGGVLIHTSWVLTAAHCVEGTKKLT------VRLGEY--DLRRRDHWELDLDIK
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GSYLKWI
                                                LPFKDWI
                                                                                                                                                                                                      WGYOSDRIKDGRRNRTFILTFIRIPLVARNECVEVMKNV---
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                                                                                                   AGIIGNT-RDACDGDSGGPMVVFFRG----
                                                                                                                                                 ASWEPTAPSDICTAETGGIAAVSFPGRASPEPRWHLMGLVSWSYDKTCSHRLSTA-FTKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----RIVNGTLTK-QG-DSPWQAILL------DSKKK--
                                                                                                   --TWFLVGLVSWG--EGCGHTNNYGIYTKV
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N;Alternate names: enterokinase enteropeptidase (EC 3.4.21.9) precursor [validated] bovine

C;Species: Bos primigenius taurus (cattle)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_chang
C;Accession: A4.3090; A48874; A6.1436
R;Kitamoto, Y.; Yuan, X.; Wu, Q.; McCourt, D.W.; Sadler, J.E.
Proc. Natl. Acad. Sci. U.S.A. 91, 7588-7592, 1994
A;Title: Enterokinase, the initiator of intestinal digestion,
A;Reference number: A43090; MUID:94329561; PMID:8052624 #text_change 09-Jul-2004

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mosaic

protease

comp

A;Status: A; Accession: A43090 nucleic acid sequence not shown; translated from GB/EMBL/DDBJ

A; Molecule type: mRNA

A;Residues: 1-1035 <KIT>
A;Cross-references: UNIPROT:P98072; UNIPARC:UPI000004BBB5;
A;Experimental source: small intestine GB:U09859; NID:g746410;

E.A.;

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×.L.;

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catalytic

subunit

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R;LaVallie, E.R.; Rehemtulla, A.; Racie, L.A.; DiBlasio, J. Biol. Chem. 268, 23311-23317, 1993
A;Title: Cloning and functional expression of a cDNA enc. A;Reference number: A48874; MUID:94043122; PMID:8226855 of a cDNA encoding PMID:8226855

A; Accession: A48874

A;ACCESSIV.....ANA A;Molecule type: mRNA A;Residues: 801-1035 <LAV> A;Residues: 801-1035 <LAV> A;Cross-references: UNIPARC:UPI000011133D; GB:L19663; NID:g416131; PIDN:AAA16035.1; A;Cross-references: UNIPARC:UPI000011133D; GB:L19663; NID:g416131; PIDN:AAA16035.1; A;Note: parts of this sequence, R;Light, A.; Janska, H.
J. Protein Chem. 10, 475-480, 1 Con

sequence of the catalytic subunit MUID:92189715; PMID:1799406

of,

bovine

enterokinase

1991

A; Accession: A61436 A; Reference number: A61436;

of the intestinal brush

borde

C;Comment: Co C;Complex: ma lfide linked A, Molecule type: protein
A, Residues: 801-807, 'Y', 809-827 <LIG>
A, Cross-references: UNIPARC:UPI0001468A0
C; Comment: The mechanism of association with the membrane o embrane attachment using a signal-anchor sequence.
C; Comment: Conversion from membrane-bound to soluble forms
C; Complex: mature enteropeptidase is variously reported to may involve contain two (heavy and light)

C; Function:

A;Description: cleaves propeptide from trypsinogen to produce active trypsin A;Pathway: intestinal digestive hydrolase caseade C;Superfamily: enteropeptidase; C1C1s repeat homology; LDL receptor ligand-bind C;Keywords: glycoprotein; hydrolase; intestine; serine proteinase; transmembrane F;22-38/Domain: transmembrane #status predicted <TMM>
F;52-117/Product: enteropeptidase mini chain #status predicted <MCH> receptor ligand-binding

protein

;118-800/Product: enteropeptidase heavy chain #status predicted <HCH>

```
coagulation factor Xa (EC 3.4.21.6) precursor - chicken

N;Alternate names: virus-activating proteinase

C;Species: Gallus gallus (chicken)

C;Date: 12-Feb-1993 #sequence revision 07-Feb-1997 #text_change 09-Jul-2004

C;Accession: S15838; S20380; $\overline{5}20381$

R;Suzuki, H.; Harada, A.; Hayashi, Y.; Wada, K.; Asaka, J.; Gotoh, B.; Ogass

FEBS Lett. 283, 281-285, 1991

A;Title: Primary structure of the virus activating protease from chick embry

A;Reference number: S15838; MUID:91257322; PMID:2044767

A;Accession: S15838

A;Farnic Ter-
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F;358-520/Domain:
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                      ,Status: not compared with conceptual
,Molecule type: mRNA
,Residues: 1-475 <UZ>
,Cross-references: UNIPROT:P25155; UN
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Best Local Similarity
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    Yamauchi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SYPNOAFCIWNLNAQKGKNIQLHF----QEFDLENIADVVEIRDGEGDDSLFLAVYTG--
                                                                                                                                                                                                                                                                                                                                                                                                            GDSGG-----PLMCQENNRWILLAGVTSFGYQCALPNR-PGVYARVPRFTEWIQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                  AETGGIAAVSFPGRASPEPRWHLMGLVSWSYDKTCSHRLSTAFTKVLPFKDWIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SAIILHPNYDPILLDADIAILKLLDKARISTRVQPICLAASRDLSTSFQESHI-TVAGWN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RAPSCIPI-----CGK--IENITAPKTQG-----LRWPWQAAIYRRTSGVHDGSLHKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AFSKQKLQSAPTKKPALPFGDLPMGYQHLHTQLQYECISPFYRRLGSSRRTCLRTGKWSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SYVLSGNEKRTCQQNGEWSGKQPICIKACREPKISDLVRRRVLPMQVQSRETPLHQLYSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YKCACLAGYTGORCENLLEERNCSDPGGPVNGYQKITGGPGLINGRHAKIGTVVSFFCNN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RPAPIQSIGSS----LHVLFHSDGSKNFDGFHAIYBEITACS-SSPCFHDG-TCVLDKAGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SYPLNAHCEWTIHAKPGFVIQLRFVMLSLEFDYMCQYDYVEVRDGDNRDGQIIKRVCGNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ALI---YQGSTADVLQEADVPLLSNEKCQQQMPEY----NITENMVCAGYE-AGGVDSCQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VLADVRSPGFKNDTLRSGVVSVVDSLLCEEQHEDHGIPVSVTDNMFCASWEPTAPSDICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DQIVINPHYNKRRKNNDIAMMHLEMKVNYTDYIQPICLPEENQV---FPPGRICSIAGWG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AWFLVCSGALVNERTVVVAAHCVTDLGKVTMIKTADLKVVLGKFYRDDDRDEKTIQSLQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----GLGTGNSSVPTFSTGGGP--YVNLNT-----APNGSLILTPSQQCLE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -ECIPLVNL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -PGPVNDVFSTTNRMTVLFITDNMLAKQGFKANFTTGYGLGIPEPCKEDNFQC---KDG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --DSLILLQCNYKSCGKKLVTQEVSPKIVGGSDSREGAWPWVVALY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -OVCGASLVSRDWLVSAAHCV--YGR--NMEPSKWKAVLG-LHMASNLTSPQIETRLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8.0%; Score 317.5; DB 1; llarity 24.6%; Pred. No. 1.5e-13; Conservative 80; Mismatches 225;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LDL receptor ligand-binding repeat homology <LDL1> MAM homology <MAM>
  UNIPROT:P25155; UNIPARC:UPI000012A408; DDBJ:D00844; hi, F.; Ogasawara, T.; Nagai, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----ACAEN--WT-----TQISDDVCQLL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CDGFPHCKDGSDEAHCVRLFNGTTDSSGLVQFRIQSIWHV-----
                                                                                        translation
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                                                                                                                                                                                         B.; Ogasawara,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                               1031
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                      NID:g222869;
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C; Superfamily: cc
C; Keywords: beta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Accession: S20381
A; Molecule type: pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: protein A; Residues: 41-55 < GO2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Function:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    183 EVRDGDNRDGQIIKRVCGNERPAPIQSIGSSLHVLFHSDGSKNFDGFHAIYEEITACSSS
  682
                                         388
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 8.0%;
Similarity 22.2%;
                                                                                                                                                                                                                                     SVILPTNSNTNATSDQDVPSTNGSILEEVFTTTTESPTPP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PCFHDGTCVLDKAGSYKCACLAGYTGQRCENLLEERNCSDPGGPVNGYQKITGGPGLING
                                                                                 -- VVDSLLCEEQHEDHGIPVSVTDNMFCASWEPTAPSDICTAETGGIAAVSFPGRASPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PCHYGGQC-KDGLGSYTCSCLDGYQGKNCEFVIPK------YCKINNGD-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMKQGN-----IERECNEERCSKEEAREA-----FEDNEKT-EEFWNIYVDGDQCSSN
                                                                                                                                                                     DLSTSFQESHITVAGWNVLADVRSPGFKNDTL---RSGVVS-----
                                                                                                                                                                                                             EVDREKEEHSETTHTAE--KIFVHSKYIAETYDNDIALIKLKEPIQFSEYVVPACLPQA-
                                                                                                                                                                                                                                                                                                                                            AAIYRRTSGVHDGSLHKGAWFLVCSGALVNERTVVVAAHCVTDLGKVTMIKTADLKVVLG
                                                                                                                                                                                                                                                                                                                                                                                      ----PRNGSS----
                                                                                                                                                                                                                                                                                                                                                                                                                              SPFYRRLGSSRRTCLRTGKWSGRAPSCIPICGKIENITAPKTQGL-----RWPWQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -RVLPMQVQSRETPLHQLYSAAFS-KQKLQSAPTKKPALPFGDLPMGYQHLHTQLQYECI
  RWHLMGLVSWSYDKTCSHR-LSTAFTKVLPFKDWIERNMK 720
                                       VPYVDRSTCKQSTN----FAITENMFCAGYE-TEQKDACQGDSGG-----
                                                                                                                                                                                                                                                                                                   AVLIN-----EKGEEF--CGGTILNEDFILTAAHCIN-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RHAKIGTVVSFFCNNSYVLSGNEKRTCQQNGEWS--GKQPICIKACREPKISDLVRR---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   coagulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -CEQFCSIKKSVQKDVVCSCTSGYELAEDGKQ--CVSKVKYPCGKVLMKRIKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 79;
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Pred. No. 1e-13; Mismatches

177;

Indels

195;

Gaps

242

93

-DFANEVLMNQKSGMVSGFGREFEAGRLSKRLKVLE

623 352 ITDPNVDTRIVGGDECRPGECPWQ

-QSKEIKVVVG

295 525 255

225

465

415

185

357 135

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F;21-40/Domain: bropeptide #status predicted <PRO>
F;25-84/Domain: Gla domain homology <GLA>
F;25-84/Domain: Gla domain homology <GLA>
F;41-185/Product: coagulation factor X light chain #status experimental <LCH>
F;90-121/Domain: EGF homology <EG1>
F;129-167/Domain: EGF homology <EG2>
F;186-475/Product: coagulation factor X heavy chain #status predicted <HCH>
F;186-240/Domain: activation peptide #status predicted <APT>
F;186-240/Domain: trypsin homology <TRY>
F;241-475/Product: coagulation factor Xa heavy chain #status experimental <AHC>
F;241-466/Domain: trypsin homology <TRY>
F;241-466/Domain: trypsin homology <TRY>
F;461-466/Domain: trypsin homology <TRY>
F;461-466/Domain: trypsin homology <TRY>
F;461-467,74,56,59,60,65,66,69,72,75,79/Modified site: gamma-carboxyglutamic acid F;196-207,228,285/Binding site: carbohydrate (Asn) #status predicted F;196,207,228,285/Binding site: carbohydrate (Asn) (covalent) #status predicted F;282,328,425/Active site: His, Asp, Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: protein
A;Residues: 241-246,'X',248-251,'X',253-261
A;Cross-references: UNIPARC:UPI00000FCE9E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Title: Isolation of factor Xa from chick embryo as the amniotic endoprotease responsil A;Reference number: S20380; MUID:92164779; PMID:1537403 A;Accession: S20380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Description: catalyzes the proteolytic activation of prothrombin to thrombin in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEBS Lett.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology; keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutau;1-20/Demain: signal sequence #status predicted <SIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        296,
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    Score 314.5;
DB 1;
    Length 475;
                                                                                                                                                                                                                                       ,396-410
                                                                                                                                                                                                                                                                                       (Glu)
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# 4
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Qy 458 QGLR 	Db 568	559 559	525 525	Qy 251 VL : Db 465 IRKDLRCDGWA	Qy 196 KRVCGNERPAP :: Db 407 EKFCGERSQFV	Qy 140 LLESYPLNAHC Db 359HYPPNINC	Qy 82 HPGCTIFENCKSCR Db 324 HPGFEATFFQLPKM	Query Match 7.9%; Best Local Similarity 21.4%; Matches 151; Conservative 7	L L. M	Molecule Residues: Cross-ref Cross-ref Comment: f specifi al migrat	A; Molecule type: mRNA A; Residues: 1-855 < KIS> A; Cross-references: UNIPR A; Experimental source: st R; Satomi, S.; Yamasaki, Y Biochem. Biophys. Res. Co A; Title: A role for membr A; Reference number: JC777 A; Contents: Small intesti A; Accession: JC7775	RESULT 15 JC7731 membrane-bound arginine-specific C;Species: Rattus norvegicus (No C;Date: 14-Dec-2001 #sequence re C;Accession: JC7731; JC7775 R;Kishi, K.; Yamazaki K.; Yasud J. Biochem. 130, 425-430, 2001 A;Title: Characterization of a m A;Reference number: JC7731; MUID A;Accession: JC7731
QGLR	DLPMGYQHLHTQLQYECISPFYRRLGSSRRTCLRTGKWSGRAPSCIPICGKIENITAPKT 	KQPICIKACREPKISDLVRRRVLPMQVQSRETPLHQLYSAAFSKQKLQSAPTKKPALPFG : CDNVNAVSC	DPGGPVNGYQKITGGPGLINGRHAKIGTVVSFPCNNSYVL- 	VL	KRVCGNERPAPIQSIGSSLHVLFHSDGSKNFDGFHAIYEEITACSSSPCFHDGTC ::	LLESYPLNAHCEWTIHAKPGFVIOLRFVMLSLEFDYMCQVDYVEVRD	NGSWGGTLDDFYVKGFYCAECRAC 	DB 2; Le .4e-13; es 227;	p1 .on: basolateral cell surface .y: membrane-bound arginine-specific serine p	DDBJ:AB03789 ved, type II rushborder me	NA KIS> UNIPROT:Q9JJI7; UNIPARC:UPI00000E8ACO; UNIPROT:Q9JJI7; UNIPARC:UPI00000E8ACO; ce: strain Male, 7-week-old aki, Y.; Tsuzuki, S.; Hitomi, Y.; Iwana es. Commun. 287, 995-1002, 2001 membrane-type serine protease (MT-SPI) JC7775; PMID:11573963 ntestine	iffic serine proteinase s (Norway rat) ce_revision 14-Dec-2001 ce_revision 1.; Yahagi, N.; 201 f a membrane-bound argin MUID:21421307; PMID:115
WPWQAAIYRRTSGVHDGSLHKGAWFLVCSGALVN 495	APSCIPICGKIENITAPKT 457 	FSKQKLQSAPTKKPALPFG 397	SFFCNNSYVLSGNEKRTCQQNGEWSG 337	ERRNCS 281 WVCDSVNDCGDGSDEEGCS 524	TACSSSPCFHDGTC 250 : :	-CQYDYVEVRDGDNRDGQII 195 		Length 855; Indels 250; Gaps 33;	proteinase	1898 I integral membrane serine proteas membranes. It also participates in	8ACO; DDBJ:AB049189 Iwanaga, T.; Fushiki, T. -SP1) in intestinal epithelial turn	precursor - rat #text_change 09-Jul-2004 Ichinose, M.; Tsuchiya, Y.; Athauda, ine-specific serine protease from ra

DЬ	γQ	В	δ.	Дb	Q Y	Db	Ş
813 EKDGRIFQAGVVSWGEGCAQRNKPGVYTRIPEVRDWIK 850	672 SFPGRASPEPRWHLMGLVSWSYDXTCSHRLST-AFTKVLPFKDWIE 716	759 GALILOKGEIRVINOTTCEELLFQQITFRMMCVGF-LSGGVDSCQGDSGGFLSSV 812	613 KNDTLRSGVVSVVDSLLCEEQHEDHGIPVSVTDNMFCASWEPTAPSDICTAETGG-IAAV 671	704 NDETEDYDIALLELEKPAEYSTVVRPICLPDNTHVFPAGKAIWVTGWGHTKEGGT 758	553 DPILLDADIAILKLLDKARISTRVQPICLAASRDLSTSFQESHITVAGWNVLADVRSPGF 612	648 PDWLVSAAHCFQDETIFKYSDHTMWTAFLG-LLDQSKRSASGVQEHKLKRITHPSF 703	496 ERTVVVAAHCVTDLGKVTMLKTADLKVVLGKFYRDDDRDEKTIQSLQISAIILHPNY 552

Search completed: April 4, 2007, 21:57:44 Job time: 50 secs

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Perfect score:
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                     Human PRO polypeptide sequer WO200168846
                                                                       ABG95869 standard; protein; 'Human secreted/transmembrane
                                                                                                                                     WO200073454-A1.
                                                                                                                                                        AAB65218 standard; protein;
Human PRO1344 (UNQ699) prote
                                                                                                                                                                                                                        08-MAR-2001
                                                                                                                                                                                                                                           Human PRO1344.
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                                                                                                                                                                                                                                                    AAB87544 standard;
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   ABU58484
                                                     29-AUG-2002
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                                                               JS2002119130-A1.
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    ABU85662 standard; protein;
Human PRO polypeptide #85.
US2003036140-A1.
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Human PRO1344 polypeptide.
US2002103125-Al.
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US2003003531-A1.
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US2003032137-A1.
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US2003032139-A1.
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US2003027262-A1.
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               ABR74012 standard;
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Human secreted p
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Human secreted polypeptide PRO1344,
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ABO16959 standard;
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Auman secreted polypeptide PRO1344,
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Human secreted polypeptide PRO1344,
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US2003068740-A1.
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US2003049740-A1.
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US2003054458-A1.
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Human secreted poly
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US2003068736-A1.
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Human secreted poly
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Human secreted poly
US2003073171-A1.
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Human secreted polypeptide |
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                                 ABO51472 standard; protein;
Human PRO polypeptide #85.
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Human secreted poli
US2003040078-A1.
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Human secreted pol:
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Human secreted poli
US2003040059-A1.
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US2003064449-A1.
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US2003032132-A1
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Juman secreted polypeptide PRO1344,
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                                                             ABM19930 standard;
Human secreted poly
US2003104554-A1.
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Human secreted polypeptide |
US2003104545-A1.
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US2003068696-A1.
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Human secreted poly
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US2003104541-A1.
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Human secreted polypeptide PR01344,
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US2003032133-A1.
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Human secreted poly
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US2003040053-A1.
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US2003049752-A1.
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Human secreted polypeptide
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US2003073170-A1.
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US2003068686-A1.
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Human secreted polypeptide
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Human secreted/transmembrane US2003064459-A1.

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US2003104544-A1.
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US2003096357-A1.
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US2003068762-A1.
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US2003068761-A1.
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US2003068771-A1.
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US2003049681-A1.
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24-JUL-2003.
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US2003180048-A1.
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US2003181678-A1.
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US2003181671-A1.
25-SRD-2000
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                                                ADL93722 standard; protein; 720 AA.
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US2003073821-A1.
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Novel human secreted and transmembrane
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US2003215912-Al.
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Novel human secreted
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Human secreted/transmembrane
US2003211574-A1
13-NOV-2003.
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Human secreted/transmembrane
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13-NOV-2003.
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Novel human secreted and transmembrane
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         US2003180853-A1.
25-SEP-2003.
                                      ADH06438 standard;
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US2003180857-A1.
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US2005059102-A1.
17-MAR-2005.
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US2004058411-A1.
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US2003186407-A1.
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US2004091959-A1.
13-MAY-2004.
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(WATA/) WATANNABE C K
(WOOD/) WOOD W I.
                                   Human secreted polypeptide i US2006073545-Al.
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Human secreted polypeptide PRO1344,
US2006074226-A1.
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Human POLYX polypeptide #13
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Best Local :
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                                                                                                                                                                                                                                                                                                                      Human protein sequence EP1074617-A2.
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                                                                                                                                       Antipsoriatic pr
WO2004028479-A2.
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ry Match 99.4%;

t Local Similarity 97.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human regeneration-associated muscle JP2005073574-A.
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US2006141575-A1.
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Human TANGO 215 pro
WO200018904-A2.
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(SMIT/)
(RAST/)
                                                    ADS85034 standard;
Human atopic dermat
WO2004031386-A1.
                                                                                                                                                            ADN04640 standard;
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Human heat mitochondrial pr
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                                                                                                                                                                                                                                                         ADJ69990 standard;
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                   (GENO-) GENOX RES INC
                                                                                                                                                                                                   (MITO-) MITOKOR.
(BUCK-) BUCK INST
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th 99.4%;
Similarity 97.6%;
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SMITHSON
RASTELLI
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n 99.5%; Score 3926.5; DB 9
Similarity 97.7%; Pred. No. 1.9e-203;
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                                 GENOX RES INC.
                                                              ndard; protein; 737 dermatitis-related
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Pred. No. 3.6
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Pred. No. 3.6e-203;
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No. 46
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No. 3
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No. 5.
3921.5; DB 8
No. 3.6e-203;
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No. 3.6e-203;
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3.6e-203;
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3.6e-
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.9e-204;
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-203;
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Human TANGO 215 ma
US2006141575-A1.
                                                                                                                        Murine TANGO 215
US2006141575-A1.
                                                   AAE19180 standard; protein;
Human protease, PRTS-17 prot
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(HELI-) HELIX RES
                                                                                                                                                                                                                                                                                                                                                                                  AEI68141 standard; protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mouse regeneration-associated JP2005073574-A.
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WO200109349-A1.
                                                                               (MILL-) MILLENNIUM PHARM INC.
ry Match 91.0%;
t Local Similarity 89.9%;
                                                                                                                                            AEI68169 standard; protein;
                                                                                                                                                                                                                    Murine TANGO
                                                                                                                                                                                                                            AAB09927 standard;
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WO2004031386-A1.
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ry Match 97.0%;
t Local Similarity 99.7%;
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MILLENNIUM BIOTHERAPEUTICS INC.
91.3%; Score 3602.5;
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  Similarity
                  INCYTE GENOMICS INC.
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91.7%; Score 3617; DB 9;
milarity 90.3%; Pred. No. 8.9e-187;
                                                                                                                                                                                                               ndard; protein;
215 protein.
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protease-like protein
a1
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91.7%;
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protein SEQ
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90.1%;
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90.1%;
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No. 3
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No. 3.6e-
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No. 2.
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No. 1.7e-186;
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No. 8.
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.9e-187;
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.7e-198;
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Human gene 5 encoded secreted p
WO200218435-A1.
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Human polypeptide
WO200153312-A1.
                                                                                                            Therapeutic protein US2006084794-A1.
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Human CD-like molecule
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WO200061774-A2.
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                                                           ADL06662 standard;
                                                                                                                                                             (ROSE/) ROSEN C A. (HASE/) HASELTINE
                                                                                                                                                                                                                                                                                                              (HUMA-) HUMAN GENOME
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        SHANGHAI XINSHIJIE GENE TECHN DEV h 52.2%; Score 2059; Similarity 95.6%; Pred. No. 4.5
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cule HSXDF41,
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74.6%;
99.3%;
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61.2%;
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74.7%;
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No. 1.9e-158;
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No. 6.2e-131;
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        DEV CO LTD.
9; DB 7;
4.5e-103;
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9.4e-151;
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.2e-122;
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.2e-122;
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SG42456-A1
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Human polypeptide
WO200153312-A1.
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Human EST encoded |
WO200154477-A2.
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Human gene 5 encode
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WO2003002976-A2.
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WO200177137-A1.
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(ROSE/) ROSEN C A.
(HASE/) HASELTINE W
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e crab factor (
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related therapeutic
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L2-JAN-1999.
(UYSI-) UNIV SINGAPORE NAT.
16.9%;
16.9%;
16.9%;
25.4%;
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WO9915676-A1.
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WO2003002976-A2.
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ry Match 16.9%;
t Local Similarity 25.4%;
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Horseshoe crab Factor C protein !
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Horseshoe crab Factor C.
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Horseshoe crab Factor C prot
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CY Match 16.9%;
Local Similarity 25.4%;
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ry Match 16.9%;
Local Similarity 25.4%;
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N-terminally truncated Horseshoe crab
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rseshoe crab Factor
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Best Local Similarity RESULT 729
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16-NOV-1999.
(UYSI-) UNIV SINGAPORE NAT.
16-9%;
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WO200127289-A2.
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                                                                                                             Human MBL-associated serine RP1744E77 **
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Human 5' EST secreted prote
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Human polypeptide
WO200153312-A1.
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Horseshoe crab Factor C.
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Human P100 serine p
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US2005158297-A1.
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(HYSE-) HYSEQ INC.
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WO200171004-A2.
27-SEP-2001.
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Human mannose binding l
WO2004024925-A2.
25-MAR-2004.
                                                                                                                                                                                                                                                                                                   Human MBL-associated serine EP1344533-A1.
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WO200140451-A2.
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Human mannose binding
                                AEF03476 standard;
Mature rat MASP-2.
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Human MASP-1 protein,
US2005158297-A1.
                                                                                                  Murine Clr protein.
KR2001077614-A.
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UNIV LEICESTER.

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RESULT 742
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                                           AEB13349 standard; protein; Complement component Clr SEQ WO2005061537-A2.
                                                                                                                Human complement WO2003072827-A1.
                                                                                                                                                                                                                                                                    Complement complewers wo200175177-A2.
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Full length Murine
WO2005123128-A2.
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Full length rat MA
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WO2005123128-A2.
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                                                                                                                                   ADP65211 standard;
                                                                                                                                                                    (BIOC-) BIO CLUE (KIMT/) KIM T Y.
                                                                                                                                                                                                                AAG80757 standard;
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(THIE/) THIEL S.
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h 10.2%; Score 403.5;
Similarity 22.9%; Pred. No. 1.1
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(MASP-2)

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US2005158297-A1.
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Human mannin-binding lectin
US2002082208-A1.
                    AEF03426 standard;
Full length MASP-2
                                                                21-JUL-2005.
(JENS/) JENSENIUS J
(THIE/) THIEL S.
                                                                                                                                                                 09-JUN-2005
                                                                                                                                                                        Alzheimer's disease US2005123962-A1.
                                                                                                                                                                                          AEA17053 standard;
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27-JUN-2002.
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24-JAN-2002.
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                                                                                                                                                                                                                                                                                                        (JENS/) JENSEN
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(THIE/) THIEL S.
                                                                                                                                                                                                                                                                                                                                                                                                                                          AAE14564 standard;
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US2005255114-A1.
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(THIE/) THIEL S.
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US2005158297-A1.
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WO200206460-A2.
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Human MBL-associated serine
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(NATL-) NATLMMUNE
                                              WO2005123128-A2.
                                                        Mature MASP-
                                                               AEF03427 standard;
                                                                                                    (JENS/) JENSENIUS
(THIE/) THIEL S.
                                                                                                                                                   NEB26838 standard;
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(NATL-) NATLMMUNE AS.
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                (UYLE-) UNIV LEICESTER
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Human MBL-associated serine
WO2005123776-A1.
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ADE56418 standard;
Rat Protein D88250,
WO2003016475-A2.
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Novel cell pain re
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                                                                       Novel cell pain
WO2005014849-A2.
                                                                                                                                                         WO2003016475-A2.
                                                                                                                                                                 ADE83526 standard; protein; Rat Protein BAA25797, SEQ ID
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(THIE/) THIEL S.
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(FARB ) BAYER
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SEQ ID NO 2271.
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EP1394274-A2.
03-MAR-2004.
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Human Clq-associated serine
US2005158297-Al.
21-JUL-2005.
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                                  ADL91020 standard; protein; (Human mannose binding lectin WO2004024925-A2.
                                                                                                                                                                                     ADP65315 standard; protein; Human complement c1s compone
                                                                                                                 ADJ75392 standard; protein; 688 AA.
Marker gene related amino acid seq.
                                                                                                                                                                             Human complement WO2003072827-A1.
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(FARB ) BAYER
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(FARB ) BAYER AG.
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Q9UCV3, SEQ ID
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06-MAY-2005.
(NOVS ) NOVARTIS AG.
(NOVS ) NOVARTIS PHARMA GMBH.
(NOVS ) NOVARTIS PHARMA GMBH.
8.5%; S
Match
221.7%; F
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Human NOVX protein
WO200268649-A2.
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(HERM/) HERMANN K.
(CAST/) HEIDEN CASTANOS-VELEZ
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Human NOVX protein
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WO2004030615-A2.
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                                                                                                WO200268649-A2.
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                Human prostamin,
US2006009634-A1.
                                                                                                                                                                      06-SEP-2002
                                                                                                                                                                                                                                       (COMP-) COMPUGEN LTD.
                                                                                                                                                                                                                                                                     AEK17066 standard;
Human C1S fragment
WO2005072340-A2.
                                                                                                                                                                                                                                                                                                                                (NUVE-) NUVELO INC
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                                     AEF27702 standard;
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                                                                                                                                                         (CURA-) CURAGEN CORP.
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antigenic
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ID NO:1533.
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W02005110338-A2.
24-NOV-2005.
(GANY-) GANYMED PHARM AG.
uery Match 8.4%;
est Local Similarity 22.9%;
Human enteropeptidase.
WO2006050999-A2.
18-MAY-200
                                                                                                                                                                                              ADI10400 standard;
Human cell surface
WO200295007-A2.
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(CORV-) CORVAS INT
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                                                                                   AEH25673 standard; protein;
                                                                                                                                 Human transmembrane US2004001801-A1.
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(CORV-) COR
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AAU11812 standard; protein; Cancer and neurogenesis assow0200190354-A1.
                                                                          AAU11813 standard; protein; Cancer and neurogenesis assow0200190354-A1.
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Human protein of the
WO2003102155-A2.
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(UYLE-) UNIV LEEDS
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ry Match 8.3%;
t Local Similarity 20.8%;
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(BUCK-) BUCK INST AGE
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ID AAB19552 standard;
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       Human matriptase. WO200053232-A1.
                                                                                                                                                                                                                                                   AAM25628 standard; protein;
Human protein sequence SEQ
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Human peptidase, HPEP-1 prot
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Human matriptase (truncated
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                                                                                   WO2004032842-A2.
                                                                                              Protein
                                                                                                      ADO55145 standard;
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                                                                                                                                                                                  ABB11428 standard;
                                                                                                                                                                                                                                           Human protein sequence WO200153455-A2.
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WO200042201-A2.
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WO200053232-A1.
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Best Local Similarity
RESULT 815
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PRO polypeptide SEQ ID NO:428.
WO2004041170-A2.
21-MAY-2004.
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Antipsoriatic protein
WO2004028479-A2.
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Human NOVX protein
          Human prostatic carcinoma WO2004076614-A2.
                                                                                                    Human cancer-associated WO2006068975-A2.
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                                                                      (ABGE-) ABGENIX INC
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.5e-09;
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Tumour antigen derived gene
           Human membrane-type WO200157194-A2. 09-AUG-2001. (CORV-) CORVAS INT I
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(CURA-) CURAGEN CORP.
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                                               AAE06930 standard; protein;
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(UYAR-) UNIV ARKANSAS.
                                                                                                          WO200129056-A1.
                                                                                                                  Human TADG-15
                                                                                                                            AAB98500 standard;
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(UYAR-) UNIV ARKANSAS.
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WO200055180-A2
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ROSENTHAL A.
HERMANN K.
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Human NOVX protein
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Human NOVX protein
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Transmembrane serine
WO2003004681-A2.
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Human membrane-type serine p
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WO200292841-A2.
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                                                                                                              Rat C3b/C4b complement recepw0200210199-A2.
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WO2003031585-A2.
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Wild type human mem
WO2005110453-A2
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Human membrane-type serine p
WO2005100556-A2.
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Human transmembrane serine protease
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WO2004005471-A2.
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ry Match 8.3%; Score
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                                                                                 AAU99088 standard; protein; 419 AA.
Human Protein C zymogen protein mutant G383N/G385T
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WO200210199-A2.
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WO200210199-A2.
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AAU99080 standard;
Human Protein C zym
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(MAXY-) MAXYGEN HOLDINGS LTD.
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WOLENC A R.
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FURTAK K.
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ALSOBROOK J E
LEPLEY D M.
RIEGER D K.
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MILLER C
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                                                                                                                                AMGEN INC.
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zymogen protein
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Pred. No. 2
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AA.
mutant L349N/D351T
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WO2003102155-A2.
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                                                  Human protein of the WO2003102155-A2.
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Human Protein C zymogen prot
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                                                           ADH71166 standard; protein; 3104 AA.
Human protein of the invention NOV4p
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                                                                                                                                                                                                                                                                                                                                                                                                         ABG79169 standard; protein;
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                              (CURA-) CURAGEN CORP.
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(CURA-) CURAGEN CORP.
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HOLDINGS LTD.
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ADH71138 standard; protein; 3104 AA

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Human C3b/C4b compl
WC200210199-A2.
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Human Protein C zym
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WO200210199-A2.
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WO9416083-A1.
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Human protein C variant #2.
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WO200232461-A2.
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                                                                                                                                                                                                                                                                                                      AAR57283 standard; protein;
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                                                        Human Protein
                                                                 AAU99076 standard;
                                                                                                       (AMGE-) AMGEN INC
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(MAXY-) MAXYGEN HOLDINGS LTD.
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RESULT 879
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Human Protein C zymogen prot
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                                                    WO9309804-A1.
                                                                Protein C
                                                                                                                                          Human protein
US5358932-A.
                                                                                                                                                                                                                                                    AAU99079 standard; protein; 419
Human Protein C zymogen protein
                                                                                                                                                                                                                                                                                                                                           WO200232461-A2.
                                                                                                                                                                                                                                                                                                                                                       Human Protein
                                                                                                                                                                                                                                                                                                                                                                 AAU99087 standard;
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(MAXY-) MAXYGEN HOLDINGS LTD.
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WO200232461-A2.
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Human Protein C zymogen prot
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                                                                          AAR35760 standard;
                                                                                                                                                                                                           (MAXY-) MAXYGEN
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(MAXY-) MAXYGEN HOLDINGS LTD.
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(MAXY-) MAXYGEN HOLDINGS LTD.
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(MAXY-) MAXYGEN HOLDINGS LTD.
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(MAXY-) MAXYGEN HOLDINGS LTD.
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C zymogen protein
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8.0%;
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zymogen protein mutant L220N/R222T
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23.3%;
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protein mutant D351N/Q353S
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Pred. No. 4e-
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mutant G383N/G385S
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No. 3.7e-09;
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No. 3.7e-09;
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AAU99053 standard; protein;

419 AA

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RESULT
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Human Protein C zymogen prot
WO200232461-A2.
                                                                                                                                                                           ADW28523 standard; protein;
Human protein C variant #1.
WO2004113385-A1.
                                                                                                                                                                                                                                                                              ADM77504 standard; protein; Human protein C variant #2 w02003106666-A2.
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Murine NOVX
                                                                           Epithin protein.
WO200203787-A2.
                                                                                                AAE23083 standard;
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(MAXY-) MAXYGEN HOLDINGS
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          ADI16819 standard; protein; 855 AA
                                                                                                                                           (MAXY-) MAXYGEN HOLDINGS LTD (MAXY-) MAXYGEN APS.
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(MAXY-) MAXYGEN HOLDINGS LTD.
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Pred. No. 4.2e-09;
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No. 4.2e-09;
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No. 8.7e-09;
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Human protein C ana.
WO2006044294-A2.
27-APR-2006.
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(ELIL) LILLY & CO
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                                                                                                                   WO200232461-A2.
25-APR-2002.
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Human Protein C zymogen protein
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(MAXY-) MAXYGEN HOLDINGS LTD
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Human Protein C zymogen protein mutant D189N/K191S
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4.7e-09;
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25-APR-2002.
(MAXY-) MAXYGEN APS.
(MAXY-) MAXYGEN HOLDINGS LTD.
(MAXY-) MAXYGEN HOLDINGS LTD.
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Rat NOVX protein ho
WO200268649-A2.
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Rat NOVX protein ho
AAU99069 standard; protein;
Human Protein C zymogen prot
WO200232461-A2.
25-APR-2002.
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(MAXY-) MAXYGEN HOLDINGS
7.5
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(MAXY-) MAXYGEN HOLDINGS LTD.

7.9%;
                                                                                                                                                                                                                                                                                                      AAU99097 standard; protein; 419
Human Protein C zymogen protein
WO200232461-A2.
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                                                                                                                               AAU99064 standard;
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                                                                                                                                                                                                                                                                                                                                                                    (MAXY-) MAXYGEN APS.
(MAXY-) MAXYGEN HOLDINGS LTD.
                                                                                                                                                                                                                                                                                                                                                                                                      WO200232461-A2.
                                                                                                                                                                                                                                                                                                                                                                                                               AAU99072 standard; protein; 419 AA.
Human Protein C zymogen protein mutant S336N/M338T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADI16878 standard;
                                                                                                          WO200232461-A2.
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protein homologue
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mogen protein
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24.5%;
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24.2%;
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21.4%;
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23.5%;
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21.4%;
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21.4%;
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                    protein
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3 SeqID 414.
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SeqID 417.
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SeqID 356.
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Pred. No.
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Pred. No. 6
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Pred. No. 9.
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mutant
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mutant D189N/K191N
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No. 9.
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No.
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5.4e-09;
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25-APR-2002.
(MAXY-) MAXYGEN APS.
(MAXY-) MAXYGEN HOLDINGS LTD.
(MAXY-) MAXYGEN HOLDINGS LTD.
7.9%; S
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WO200232461-A2.
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Human Protein C zymogen protein
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WO200232461-A2.
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WO200232461-A2.
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Human Protein C zymogen protein
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Human Protein C zymogen prot
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                                              AAU99092 standard; protein;
                                                                                                                          AAU99075 standard; protein; 419 AA.
Human Protein C zymogen protein mutant M338N.
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Human Protein C zymogen protein
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WO200232461-A2.
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(MAXY-) MAXYGEN HOLDINGS LTD.
(MAXY-) 7.9%;
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TEY 24.5%;
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HOLDINGS LTD.
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zymogen protein mutant D351N/Q353T
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mutant H303N/S305T
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mutant L387N/N389S
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mutant L387N/N389T
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No. 5.4e-09;
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#O200232461-A2.

MAXYGEN MAXYGEN

HOLDINGS

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Query Match
Best Local S
RESULT 915
                                                                                  Query Match
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24-DEC-2003.
(MAXY:) MAXYGEN APS.
(MAXY-) MAXYGEN HOLDINGS LTD.
7.9%; S
7.9%; S
24.5%; I
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Human Protein C zymogen prot
WO200222461-50
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                                   Human Protein EP443875-A.
                                                                                                          AAB82677 standard; protein; Human protein C derivative W0200157193-A2.
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WO2005072340-A2.
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Human protein C variant #5 a
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                                                      AAR13537 standard;
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                                                                                                                                                                                                              AEK17063 standard; protein;
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protein mutant
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312; DB 2;
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WO2003082914-Al.
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WO200250105-A1.
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                                                             Human Protein
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WO200232461-A2.
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(SMIK ) SMITHKLINE BEECHAM
(GLAX ) GLAXO GROUP LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABP60993 standard;
                                                   WO200232461-A2.
                                                                       AAU99044 standard;
                                                                                                                                                                                                                                                                                                                              NO200232461-A2.
                                                                                                                                                                                                                                                                                                                                                 AAU99047 standard; protein; 419
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(MAXY-) MAXYGEN HOLDINGS LTD.
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6.3e-09;
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6.1e-09;
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AAU99014 standard;

protein;

419 AA

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RESULT 934
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RESULT 937
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Best Local S
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25-APR-2002.
(MAXY-) MAXYGEN APS.
(MAXY-) MAXYGEN HOLDINGS LTD.
(MAXY-) MAXYGEN HOLDINGS LTD.
7.9%; 5
Human protein
EP443874-A.
28-AUG-1991.
                                                                                                                                                                                                                                                                                                                                   AAU99095 standard; protein; 419 Human Protein C zymogen protein WC200232461-A2.
               AAR13997 standard; protein;
Human protein C zymogen Q329
                                                                                           AAR13539 standard; protein;
Human Protein C zymogen LIN
                                                                                                                                          04-MAY-1988.
(ZYMO) ZYMOGENETICS
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Human Protein C zymogen prot
WO200232461-A2.
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Human Protein C zymogen protein
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WO200232461-A2.
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EP266190-A.
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(MAXY-) MAXYGEN HOLDINGS
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                                                                          28-AUG-1991.
                                                                                   EP443875-A.
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Human protein C.
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AAB36896 standard; protein; 419 Human protein C derivative 3. WO200066754-Al. 09-NOV-2000.
                                                                                     AAB82673 standard; protein; Wild-type human protein C.
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Human activated pro
WO2003075834-A2.
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WO200157193-A2.
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Human protein C derivative
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                                                                                                                                                                    AAY56803 standard; protein;
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Rat factor VII.
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(ELIL ) LIL
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No. 6.7e-09;
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(MAXY-) MAXYGEN APS.

(MAXY-) MAXYGEN HOLDINGS LTD.

(MAXY-) MAXYGEN HOLDINGS LTD.

7.9%; S
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Human mature wild type protein C.
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Human Protein C zymogen
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Human Protein C zymogen protein mutant R312N/R314S
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16-AUG-2001.
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Human Protein C zymogen
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Human Protein C zymogen protein mutant
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(MAXY-) MAXYGEN HOLDINGS LTD.
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WO200232461-A2.
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(MAXY-) MAXYGEN HOLDINGS LTD.
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(MAXY-) MAXYGEN HOLDINGS LTD.
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Pred. No. 6.9e-09;
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                                               Human activated WO2003075834-A2.
                                                         ADC40014 standard; protein; 419 AA.
Human activated protein C-related p
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Amino acid sequence of mature human
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(MAXY-) MAXYGEN HOLDINGS LTD.
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h 7.9%; Score 310.5; DB 6;
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Human protein C analog with
WO2006044294-A2.
27-APR-2006.
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Human protein C and
WO2006044294-A2.
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WO2006044294-A2.
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Human protein C analog with
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Human protein C.
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                           WO2003082914-A1.
                                             ADG83834 standard;
Mainland tiger snak
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(MAXY-) MAXYGEN HOLDINGS
(MAXY-) MAXYGEN APS.
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(MAXY-) MAXYGEN HOLDINGS LTD.
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22-AUG-1991.
(ZYMO) ZYMOGENETICS I
TEIJIN LTD.
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Sequence of polypeptide with
EP191606-A.
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JP63263083-A.
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Zymogen form of human protei
                                                                                              Protein C pro
WO9109951-A.
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        JP05064588-A.
19-MAR-1993.
                         AAR34295 standard;
Protein C.
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EP323149-A.
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Human Protein C.
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(ZYMO ) ZYMO
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Human wild type protein C.
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Human protein C derivative ?
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                                      (MAXY-) MAXYGEN APS.
(MAXY-) MAXYGEN HOLDINGS
(MAXY-) MAXYGEN HOLDINGS
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(MAXY-) MAXYGEN HOLDINGS
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Human Protein C precursor protein.
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Human zymogen-like
WO2004044190-A2.
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(MAXY-)
                        PC-UGAC-GPI-4stop
WO2005073375-A1.
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                                                                                                          ABC01741 standard; protein; PCUAAC-GPI-4Stop cassette.
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WO2005073375-A1.
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(ZLBB-) ZLB
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Score 310.5;

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9,

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Query Match
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RESULT 1008
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Best Local S
RESULT 1002
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09-AUG-2001.

(ELIL ) LILLLY & CO ELI.

7.9%; (
24.5%;
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Human HUMCIRS PEA 1 P22 pro
WO2005072340-A2.
                                                                                                                                                                                                                                                        Human protein; Human protein C derivative 5 WO200066754-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                         AAR13538 standard; protein;
Human Protein C zymogen FN.
EP443875-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAE08630 standard; protein; 419 AA.
Human protein C derivative #4.
W0200159084-A1.
       AAU99013 standard;
Human Protein C zym
WO200232461-A2.
                                                                                                                                                                                   AAU99018 standard;
Human Protein C zym
WO200232461-A2.
                                                                                                                                                                                                                                                                                                                                                      AAB36897 standard; protein;
Human protein C derivative '
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB82676 standard; protein; 419 AA.
Human protein C derivative (S11G/Q32E/N33D/L194S/T254S)
                                                                                     WO200232461-A2.
25-APR-2002.
                                                                                                   AAU99033 standard; protein; 419 AA.
Human Protein C zymogen protein mutant K251N.
                                                                                                                                                                           25-APR-2002.
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HOLDINGS LTD.
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protein mutant
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No. 7.3e-09;
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No. 9e-09;
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25-APR-2002.
(MAXY-) MAXYGEN APS.
(MAXY-) MAXYGEN HOLDINGS LTD.
(MAXY-) MAXYGEN HOLDINGS LTD.
7.8%; S
                                                                                                                                      Human Protein C
WO200232461-A2.
                                 Human Protein C zymogen
                                                                                                                                                AAU99019 standard; protein; 419
Human Protein C zymogen protein
                                                                                                                                                                                                                                         AAU99058 standard; protein; 419 AA.
Human Protein C zymogen protein mutant K308N/A310T.
WO200232461-A2.
25-APR-2002.
                                                                                                                                                                                                                                                                                                                                                                      WO200232461-A2.
                                                                                                                                                                                                                                                                                                                                                                                AAU99085 standard; protein; 419
Human Protein C zymogen protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human Protein
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(MAXY-) MAXYGEN HOLDINGS LTD.
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Human Protein C zymogen protein
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Human Protein C zymogen protein mutant F316N/L318T
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(MAXY-) MAXYGEN HOLDINGS LTD.
                      WO200232461-A2.
                                              AAU99094 standard;
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(MAXY-) MAXYGEN HOLDINGS LTD.
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(MAXY-) MAXYGEN HOLDINGS LTD.
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protein mutant S252N.
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                                  mutant H388N/Y390T
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EP319312-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AEH44153 standard; protein; 419 AA.
Human protein C analog with Q353R substitution
                                                                             AAE08629 standard; protein;
Human protein C derivative
                                                                                                                                                 Human protein C derivative WO200159084-A1.
                                                                                                                                                                                                                               Murine NOVX protein WO200268649-A2.
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                                                                                                                                                                                                                                                                                                                       NDI16874 standard; protein; 79
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(MAXY-) MAXYGEN HOLDINGS LTD.
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          AAU99049 standard;
                                                                     Human protein C
WO200159084-A1.
                                                                                                                                                                      AAE08627 standard;
                                                                                                                                                                                                                                                    ADI16880 standard; protein; 799 AA
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protein
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#3.
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Pred. No. 1.4e-08;
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Pred. No. 1.
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mutant L386N/H388S
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No. 8.
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No. 7.8e-09;
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l.4e-08;
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Human Protein C zyn
WO200232461-A2.
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                                                                   ADM77506 standard;
Human protein C var
WO2003106666-A2.
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WO200232461-A2.
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        AAE08628 standard;
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(MAXY-) MAXYGEN HOLDINGS
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zymogen protein mutant K251N/T253S
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Human protein C WO200159084-A1.

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RESULT 1039
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Human protein C ana
WO2006044294-A2.
27-APR-2006.
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(MAXY-) MAXYGEN APS.
(MAXY-) MAXYGEN HOLDINGS
7.6
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25-APR-2002.
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(MAXYY-) MAXYGEN HOLDINGS LTD.
(MAXY-) MAXYGEN HOLDINGS LTD.
7.8%;
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WO200232461-A2.
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Human Protein C zymogen protein
WO2002324G1-A2
25-APR-2002
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(MAXY-) MAXYGEN HOLDINGS LTD.
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RESULT 1050

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Human protein C zymogen Q313.
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Human Protein C zymogen prot
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                Human protein EP443874-A.
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(MAXY-) MAXYGEN HOLDINGS LTD.
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No.
                                                   304.5; DB 1
No. 1.4e-08;
                                                                                                                                                                                                                                                                       305
No.
                                                                                                                                                                                                                                                                                                                                                                                                                                      306.5; DB 9
                                                                                                                                                                                                                                                                                                                                                       305.5; DB 5
No. 1.3e-08;
                                                                                                                         305; DB 9;
No. 2.1e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1.2e-08;
                                                                                                                                                                                                                                                                       1.3e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .5; DB 8;
1.3e-08;
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                                                                                                                                                                                                                                                                                 419;
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8

ELI.

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Best Local Similarity RESULT 1051
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RESULT
                         Best Local Similarity RESULT 1059
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RESULT 1052
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                                                                                                                                                                                                                                                                                   AAP93714 standard,
Hybrid protein of I
EP296413-A.
                                                                                     Mouse factor VII WO2005014775-A2.
                                                                                                                                                                                    ADX39098 standard; protein; Mouse factor VII mutant. W02005014775-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human protein C
EP443874-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR13584 standard;
                                                                                                                                                                                                                                                                                                                                                                                                            Human Protein C zymogen protein mutant
                                                                                                                                                                                                                                                                                                                                                                                                                         AAU99038 standard; protein; 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human Protein C zymogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (MAXY-) MAXYGEN APS.

(MAXY-) MAXYGEN HOLDINGS LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200232461-A2.
 AAU99041 standard;
Human Protein C zyr
                                                                                                           ADX39094 standard; protein; 446
                                                                                                                                                                                                                                                                                                                                                           (MAXY-) MAXYGEN APS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (MAXY-) MAXYGEN APS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200232461-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ANU99027 standard; protein; 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human Protein
                                                                (UYFL)
                                                                           17-FEB-2005
                                                                                                                                                             (UYFL ) UNIV FLORIDA
                                                                                                                                                                          L7-FEB-2005
                                                                                                                                                                                                                                                                                                                                                                                                  10200232461-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AU99028 standard; protein; 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AU99037 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
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                                                                                                                                  local Similarity
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                                  UNIV FLORIDA RES FOUND INC.;h 7.6%; Score Similarity 22.3%; Pred.
                                                                                                                                                                                                                                                   HOECHST JAPAN LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TILLY & CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C zymogen protein mutant V243N/V245T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C zymogen
d; protein; 419 AA.
zymogen protein mutant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 zymogen
                                                                                                                                                                                                                                                                                               protein:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ) EL1.
7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mogen Q248.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7.7%;
24.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                7.6%;
24.5%;
                                                                                                                                 RES FOUND INC.
7.6%; Score 301.5;
22.3%; Pred. No. 3.
                                                                                                                                                                                                                                    7.6%;
24.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7.78;
24.48;
                                                                                                                                                                                                                                                                                                                                    24.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7.78;
24.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ein; 419
protein
                                                                                                                                                                                                                                                                                                                                              .68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ein; 419 AA.
protein mutant V243N/V245S.
                                                                                                                                                                                                                                                                                               461
and
                                                                                                                                                                                                           681 AA.
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Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 302.5; DB 5; Pred. No. 1.9e-08;
                                                                                                                                                                                                                                    Score 301.5; DB 1;
Pred. No. 2.3e-08;
                                                                                                                                                                                                                                                                                                                                    Score 301.5; DB 5; Pred. No. 2.1e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 301.5; DB 5; Pred. No. 2.1e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 302.5; DB 5; Pred. No. 1.9e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 304.5; DB 2; Pred. No. 1.6e-08;
                                                                                                                                                                                                                                                                                               AA.
Factor-X.
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                                     300.5;
No. 2.
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No. 1.6e-08;
 D255N/D257S
                                                                                                                                                                                                                                                                                                                                                                                                            T253N/D255T
                                                                                                                                     3.3e-08;
                                     ; DB 9;
.5e-08;
                                                                                                                                               DB 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 419;
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                                                                                                                                                681;
                                                                                                                                                                                                                                               461;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        419;
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                                                446;
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Best Local Similarity RESULT 1067
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RESULT 1061
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                                      Query
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                                                                                                                                                                                                                                                                                                    Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                             Human Protein C zymogen protein mutant D255N/D257T
WO200232461-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (MAXY-) MAXYGEN HOLDINGS LTD 7.6%; Ty Match 7.6%; 24.2%;
                                                                                                                                                                                                                                                  ADB65750 standard; protein; 397 AA.
Human protein encoded by clone UTERU20087070.
                                                                                                                                                                                                                                                                                                                                       Danio factor VII. WO2005014775-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human Protein C zymogen protein mutant V245N/P247T WO200232461-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rabbit factor VII. WO2005014775-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200232461-A2.
25-APR-2002.
ADI17268 standard; protein;
                                                                                                                         Human t-plasminogen
US2006216722-A1.
                                                                                                                                     AEL57571 standard; protein; 54
Human t-plasminogen activator
                                                                                                                                                                                              (HELI-) HELIX RES INST.
(REAS-) RES ASSOC BIOTECHNOLOGY.
                                                                                                                                                                                                                                       EP1308459-A2.
                                                                                                                                                                                                                                                                                                                                                                ADX39092 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (MAXY-) MAXYGEN APS.
(MAXY-) MAXYGEN HOLDINGS LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAU99030 standard; protein; 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               #O200232461-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAU99029 standard; protein; 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADX39097 standard; protein; 443 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (MAXY-) MAXYGEN
                                                                                                                                                                                                                                                                                     (UYFL ) UNIV FLORIDA RES FOUND INC.
TY Match 7.6%; Score
Local Similarity 23.0%; Pred.
                                                                                                                                                                                                                                                                                                                                                                                                              (MAXY-) MAXYGEN APS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (MAXY-) MAXYGEN APS.
(MAXY-) MAXYGEN HOLDINGS LTD.
                                                                        TAKE/) TAKEMOTO M.
                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                          Local Similarity
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Local Similarity 24.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                      Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ) UNIV FLORIDA RES FOUND INC
                                               PATRAKKAS J.
                                                                                                  BETSHOLTZ C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         zymogen protein mutant V245N/P247S
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24.2%;
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24.0%;
                        7.5%;
23.0%;
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24.4%;
                                                                                                                                                   543 AA
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230 AA.
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Pred.
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No.
                        297.5; DB 10;
No. 4.4e-08;
                                                                                                                                                                          No.
                                                                                                                                                                                                                                                                                      298.5; DB 9;
No. 3.1e-08;
                                                                                                                                                                                                                                                                                                                                                                                        298.5; DB
No. 3e-08;
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No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  298.5; DB
No. 3e-08;
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No. 2.7e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3.5; DB
3e-08;
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2.8e-08;
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                                                                                                                                                                         DB 7;
1.1e-08;
                                                                                                                                      SEQ ID NO: 2034.
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                                                                                                                                                                                     Length 397;
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Polypeptide

homologous to a

human NOVX domain SeqID

804

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Query
Best L
RESULT 1
ADI17276 standard; protein; Polypeptide homologous to a WO200268649-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     06-SEP-2002.
(CURA-) CURAGEN
                                                                                                                                                                                                                                                                                                                                                                           Trypsin-like ser US2003170630-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200268649-A2
                                                                                                                                                     Trypsin-like ser
US2006009634-A1.
                                                                                                                                                                                                                                                                                                                                                                                        ADJ83075 standard; protein;
                                                    (EDIN/
                                                                                     (BURG)
                                                                                                                                                                  AEF27705 standard; protein;
                    (BOLD/
                                       (YALY)
                                                                                                                                                                                                                                                                                                                                                                                                                  CURA-) CURAGEN CORP.
        SHEN
                                                                                            LEPL/
                                                                                                                                          語な/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                     ocal Similarity
                            EDINGER S.
SCIORE P.
ELLERMAN K.
MALYANKAR U.
ROTHENBERG M.
STONE P.
                                                                                                                                                                                                                                 CASMAN S J.
BOLDOG F L.
GORMAN L.
GANGOLLI E A.
FERNANDES E R.
RIEGER D K.
EDINGER S R.
                                                                            PATTURAJAN M.
GROSSE W.
LEPLEY D.
BURGESS C.
VERNET C.
                                                                                                                                                                                           ELLERMAN K.
MACDOUGALL J
SMITHSON G.
                                                                                                                                                                                                                                                                                     BURGESS C E.
SHIMKETS R A.
GROSSE W M.
SZEKERES E S.
VERNET C A M.
                                                                                                                                                                                                                                                                                                                       SPYTEK K A.
ZERHUSEN B I
PATTURAJAN N
LEPLEY D M.
                                                                                                                           KEKUDA R.
ALSOBROOK J.
TCHERNEV V.
                                                                                                                                                                                                                MILLET I.
SCIORE P.
                  MALYANKAR U
ROTHENBERG |
STONE D.
BOLDOG F.
SHENOY S.
ANDERSON
      BOLDOG
GUO X.
SHENOY
                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                 TCHERNEV V
                                                                                                                                                                                                                             EDINGER S ! GUNTHER E.
                                                                                                                                                                                                                                                                                                                                                               ALSOBROOK J P.
                                                                                                                    LIU X.
                                                                                                                                                                                                                                                                                                                                                                                  Berine
                                                                                                                                                            serine
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32.3%;
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                                                                                                                                                           protease
                                                                                                                                                                                                                                                                                                                                                                                  protease
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32.3%;
                                                                                                                                                                               7.5%;
32.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                    230 AA.
human N
                                                                                                                                                                                                                                                                                                                                                                                        230 AA
                                                                                                                                                                  230 AA
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Pred.
                                                                                                                                                                               Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                  protein
                                                                                                                                                                                                                                                                                                                                                                                                     Score
Pred.
                                                                                                                                                           consensus
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No. 2.
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No. 2.
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No. 2.4e-08;
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                                                                                                                                                                                                                                                                                                                                                                                  SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                      domain SeqID
                                                                                                                                                           sequence,
                                                                                                                                                                               DB 7;
.4e-08;
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.4e-08;
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                                                                                                                                                            SEQ: 135
                                                                                                                                                                                     230;
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Query Match
Best Local Similarity
RESULT 1071
ID AEG02859 standard; pr
DE Factor VII/X fusion p
PN W02006018204-A1.
PD 23-FEB-2006
PA (ZLBB-) ZLB BEHRING G
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RESULT 1076
                                                                                                                                                                                                                                                                                                                                                                                     Dest Local Similarity
RESULT 1074
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RESULT 1072
         Best Local
RESULT 1079
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RESULT 1077
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Best Local Similarity
RESULT 1075
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Best Local Similarity
RESULT 1073
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Best I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query
                                                                                                                                                                                                                                                                             Sequence of thr 68, Gln 1 WO8912681-A.
                                                                                                                                                                                                                                       WOSSIES:
28-DEC-1989.
(BRBI-) BRIT BIO-TECHN LTD.
7.5%;
7.5%;
23.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                             Novel human diagnostic WO200175067-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (MILL/)
                                                    AAR70903 standard;
Human t-PA variant
US5385732-A.
                                                                                                                            ABU12065 standard; protein; 986 Human NOV12a CG92293-01 protein W0200281625-A2.
                                                                                                                                                                                                     ADX39099 standard;
Bovine factor VII.
WO2005014775-A2.
                                                                                                                                                                                                                                                                                                                                                                       ADX39096 standard;
Chicken factor VII.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABG21442 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mutant human plasminogen activator CN1526726-A.
                                  31-JAN-1995.
(GETH ) GENENTECH
                                                                                                                                                                                                                                                                                                         AAR09290 standard;
                                                                                                                                                                                                                                                                                                                                           17-FEB-2005.
(UYFL ) UNIV FLORIDA
                                                                                                                                                                                                                                                                                                                                                              WO2005014775-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           08-SEP-2004.
(LIBB/) LI B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADW64351 standard; protein;
AAR70895 standard; protein; 527 AA
                                                                                                                                                                                                                                                                                                                                                                                                                    (HYSE-) HYSEQ INC.
                                                                                                             (CURA-)
                                                                                                                       7-OCT-2002
                                                                                                                                                                                              7-FEB-2005
                                                                                       Local Similarity
                                                                                                    Match
                                                                                                                                                                                                                                                                                                                                                                                                            Match
                                                                                                                                                                                                                                                                                     uence of tissue 68, Gln 117).
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MILLER C
EISEN A.
                                                                                                            CURAGEN CORP.
                                                                                                                                                                                    UNIV FLORIDA
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                 Similarity
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                                    INC.
                                                              protein; 527 AA. (N103, A432, A434)
                                                                                                                                                                                                                       protein;
                                                                                                                                                                                                                                                                                               protein; 562 AA.
plasminogen activator
                                                                                                                                                                                                                                                                                                                                                                                protein;
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7.5
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23.4%; Pred.
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7.4%;
24.1%;
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                 7.4%;
23.4%;
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25.2%;
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32.3%;
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21.8%;
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23.4%;
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21.0%;
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                                                                                                                                                                  ND INC.
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#21433.
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No. 8.
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No. 4
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No. 2.4e-
                 292;
No. 8
                                                                                          293;
No. 1.
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No. 5.5
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No. 4.
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No. 5
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No. 7e-08;
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                  8.4e-08;
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.8e-08;
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.1e-08;
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.Зе-
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Query Match
Best Local Similarity
RESULT 1087
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Best Local Similarity
RESULT 1082
                                                                                                                                 Best Local Similarity RESULT 1086
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Delta (466-470) tPA variant
                    Plasmid pDAP3 encoded sequer JP61139386-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABM80985 standard; protein; Tumour-associated antigenic WO2004030615-A2.
                                                                                                                                                                                                                                                                                                                                                                                                  Human t-plasminogen
US2006216722-A1.
                                                                                                   WO2003082914-A1.
                                                                                                           ADG83838 standard; prote
Rough scale snake venom
                                                                                                                                                            (UPJO ) UPJOHN CO.
(MARO/) MAROTTI K R.
                                                                                                                                                                                                      Sequence of tissue
                                                                                                                                                                                                                AAP70475 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                     AEL57575 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human myocardial WO2004058052-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADQ39246 standard; protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADN03787 standard;
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                                                                                                                                                                                                                                                                                                                                     PATR/) PATRAKKAS J.
                                                                                UYQU ) UNIV QUEENSLAND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPL-) APPLERA CORP.
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TOYO SODA MFĞ CO LTD
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                                                                                                                     protein;
                                                                                                                                                                                                    protein; 564 AA.
plasminogen (TPA)
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22.7%;
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23.1%;
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23.1%;
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23.1%;
                                                           7.4%;
22.2%;
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22.9%;
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23.1%;
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                            sequence.
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with
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                                       516 AA
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nce #90.
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Pred.
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Pred. No. 8.
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Pred. No. 8.
                                                                                                                                                                                                                                                                                                                                                                                                            precursor,
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h H432A
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                                                         ≥ 291; DB 8;
. No. 7e-08;
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No. 8.
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No. 9.
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No.
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No.
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                                                                                                           activator,
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. 8.9e-08;
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                                                                                                                                                                                                                                            522;
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Best Local Similarity RESULT 1094
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AAR22664 standard;
tPA analogue KK2A.
US5106741-A.
21-APR-1992.
(UPJO) UPJOHN CO.
                                                                                                                                                                                                   Human tissue CN1397564-A.
                                                                                                                       AAR12340 standard;
T-PA variant contg
                                                                                                                                                                                                                         ADL00357 standard;
                                                                                                                                                                                                                                                                                                     ADW64350 standard; protein; 527 AA.
Mutant human plasminogen activator protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR70878 standard; protein; 483 AA.
Human tissue PA variant (deltal-44,N103,D184,E275)
                                                                                                                                                                                                                                                                                  08-SEP-2004.
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31-JAN-1995.
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                                                                                        (FUJI
                                                                                                                                                                                                                                                                                                                                                             (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                        AAR70894 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human tissue PA variant
US5385732-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAR70885 standard; protein;
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CENTRAL GLASS CO LTD.
HODOGAYA CHEM IND CO
                                                               FUJISAWA PHARM CO LTD.

h 7.3%; S
Similarity 22.2%; F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NISSAN CHEM IND LTD.
NISSAN CHEMICAL INDS
h 7.4%;
Similarity 23.1%;
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CENTRAL GLASS CO
TOYO SODA MFG CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SAGAMI CHEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            human tissue plasminogen activator (TPA)
                                                                                                                                                                                                             type
                                                                                                                                                                                                             plasminogen activator
                                                                                                                       protein; 559 fibronectin
                                                                                                                                                                                                                                                                                                                                                                                              protein; 527 AA. (N103, A303, A304)
                                                                                                                                                                                                                       protein; 520 AA.
                                            protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CO.
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23.1%;
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No; 1e-07;
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No. 1
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No.
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No. 1e-07;
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No. 1e-07;
                                                                289.5; DB 2
No. 1.2e-07;
                                                                                                                      thrombosis
                                                                                                                                                      1.1e-07;
                                                                                                                                                                                                                                               1.1e-07;
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.1e-07;
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7.3%;

Score 289.5;

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Length

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48:

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RESULT 1100
ID ADI1037
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PA (CORV-)
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Best Local S:
RESULT 1097
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RESULT 1101
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RESULT 1099
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Best Local
RESULT 1098
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RESULT
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                                                                                                                                 Best Local Similarity RESULT 1103
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Query
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                          AAB85076 standard; po
Amino acid sequence o
WO200140451-A2.
07-JUN-2001.
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Human cell surface
WO200295007-A2
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                                                                                                        t-PA insertion WO9002798-A.
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t-PA insertion variant i304
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US2002169284-A1.
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Human secreted/transmembrane
US2003073624-A1.
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                                              ADE49203 standard; protein; l
Human secreted/transmembrane
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27-MAR-2003.
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ADE35257 standard;

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20-NOV-2003.
(GETH ) GENENTECH INC.
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MATCh 7.771EV 22.7%;
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30-OCT-2003.
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Human secreted/transmembrane US2003104536-A1.
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(GETH ) GEN
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ADF40560 standard; protein; E
Human secreted/transmembrane
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Human secreted/transmembrane
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GERRITSEN M E.
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BAKER K P.

BOTSTEIN D.

DESNOYERS L.

EATON D L.

FERRARA N.

FILVAROFF E.
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ROY M A.
SHELTON D L.
STEWART T A.
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KUO S S.
NAPIER M A.
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GIRMALDI J C.
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protein,

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Query Match
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RESULT 1156
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                                                                                  ADF26330 standard; protein; E
Human secreted/transmembrane
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Human secreted/transmembrane
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                                                        ADG58910 standard; protein; I Human secreted/transmembrane US2004005657-A1.
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ADG62366 standard;
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08-JAN-2004.
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Human secreted/transmembrane
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Human secreted/transmembrane US2004006219-A1.

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Human PRO618 protein sequenc
AU2002317529-A1.
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Human secreted/transmembrane
US2004063921-A1.
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04-FEB-2004.
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PRO618 protein, SEQ ID 169.
US2005014226-A1.
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                                                 GODDARD A.
GODDWSKI P J.
GRIMALDI J C.
GURNEY A L.
HILLAN K J.
KLJAVIN I J.
KUO S S.
NAPIER M A.
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       PAN J.
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Best Local Similarity
RESULT 1172
ID ADZ52064 standard; p
DE Human secreted/trans
PN US2005084935-Al.
PD 21-APR-2005
PA (ASHK) ASHKENAZI A
PA (BAKE) BAKER K P.
PA (BOTS) BOTSTIEIN D.
PA (EATO) EATON D L.
PA (FILV) FILVAROFF E.
PA (FILV) FILVAROFF E.
PA (GERR) GERBER H.
PA (GERR) GERBER H.
PA (GERR) GERRITSEN M
PA (GODD) GODDARD A.
PA (GODD) GODDARD A.
PA (GODN) GODWSKI P.
PA (GURN) GRIMALDI J C.
PA (HILL) HILLAN K J.
PA (KUJS) KUO S S.
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Query Match 7.3%; Score 288.5; Best Local Similarity 21.4%; Pred. No. 2 RESULT 1177

ID AAU77549 standard; protein; 902 AA. DE Murine type II membrane serine protease,
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                                                                                     AAU80517 standard; protein; Mouse epithilin-like serine WO200196378-A2.
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                                                                                                                                                                                          Murine epithin.
W0200129056-A1.
                                                                                                                                                                                                                   AAB98507 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                              Human PRO618
                                                                                                                                                                              26-APR-2001
                                                                                                                                                                                                                                                                                                                     AEH18123 standard;
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                                                                                                                                                       Match
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ROY M A.
SHELTON D L.
STEWART T A.
TUMAS D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GODDARD A.
GODOWSKI P J
GRIMALDI J C
GURNEY A L.
HILLAN K J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DESNOYERS L.
EATON D L.
FERRARA N.
FILVAROFF E.
                                                                                                                                                                  VINU
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KUO S S.
NAPIER M A.
                                                                                                                                                                                                                                                                                                                                                                       GENENTECH INC.
                                                                BAYER
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                                                                                                                                                                                                                                                                      INC.
                                                                                                                                                                                                                                                                                                         ; protein; amino acid
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22.7%;
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protease.
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Pred.
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Pred. No. 1.9e-07;
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Pred.
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Pred. No. 1.9e-07;
                                                                                                                                         Score 288.5;
Pred. No. 2.
                                                                                                                                                                                                                                                                                                          sequence
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No. 1.9e-07;
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1.9e-07;
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epithin.

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RESULT 10 DE
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                                                                                                     Best Local Similarity
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JP03285680-A.
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Human t-PA variant
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JP03285680-A.
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EP373896-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200212461-A2.
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t-PA analogue expressed by p
                                                                                                                                                                                                                                                                                                                                      AAR20217 standard;
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tPA024 precursor protein.
                                                                                AAR70904 standard;
Human t-PA variant
                                                                                                                                                    JS5385732-A.
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(YAWA ) NIPPON STEEL
                                                                                                                                                                                                                                                                                                                                                         (SUMU ) SUMITOMO SEIYAKU KK.

CY Match 7.3%;
Local Similarity 23.2%;
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 AAY49558 standard; protein;
Human protein C protein seqn
                                                              1-JAN-1995
                                                                                                                                (GETH ) GENENTECH INC.
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N117Q, D236A,
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                                                                                                                                                                                                                                                                                                                                                                                                          protein;
                                                                                protein; 527 (N103, A440).
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(N103,A416,A417,A418).
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23.4%;
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23.2%;
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23.5%;
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; pCDM8-010.
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D238A,
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          356 AA
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Pred. No. 1.4e-07;
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Pred. No. 1
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No. 1.4e-07;
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No. 1.4e-07;
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No. 2.2e-07;
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.4e-07;
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Best Local Similarity RESULT 1187
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07-OCT-1999.
(WHED ) WHITE!
                                                                                                                                                                                                                                                                                                                                                                                                                                          ADY74310 standard; protein; Human Factor VII variant pol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADV44720 standard; protein; 406 AA.

Human factor VII mutant K143N/N145T/R315N/V317T
W02004110469-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human factor VII WO2004000366-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAM52187 standard; protein; 406 AA.
Human FVII mutant K143N/N145T/R315N/V317T
                                                                                                                                                                                                                                                                AAR13918 standard; protein;
Delta (466-470) tPA variant
                                                                                                                                                                                                                                                                                                                                                    AEF15066 standard; protein; 406 AA. Variant human coagulation Factor VII protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADJ56078 standard; protein;
Human factor VII polypeptide
AAR70879 standard; protein; 483 AA.
Human tissue PA variant (deltal-44,N103,S184,E275)
                                                                                     Coastal taipan venom
                                                                                                 ADG83828 standard;
                                                                                                                                                                                    ABP43952 standard;
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(GETH ) GEN
                                                                                                                                                                                                                                                     Delta (466-470)
WO9113149-A.
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                                                                                                                                          HYSE-) HYSEQ INC
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22.9%;
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23.0%;
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with K416A,
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No. 1.2e-07;
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No. 1.2e-07;
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1.2e-07;
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31-JAN-1995

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Human tissue
US5385732-A.
31-JAN-1995.
                                                                                                                                                                                                                                                                           Human tissue
US5385732-A.
31-JAN-1995.
                                                                                                                                                                                           AAR70882 standard; protein; 483 AA.
Human tissue PA variant (deltal-44,N103,R252,E275)
US5385732-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human tissue
US5385732-A.
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Human tissue PA variant (deltal-44,N103,E275)
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31-JAN-1995.
(GETH ) GENENTECH INC.
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Human tissue PA variant (deltal-44,N103,
US5385732-A.
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US5385732-A.
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Human tissue PA variant (delta1-44,N103,K210,E275)
                 AAR70888 standard; protein; 483 AA.
Human tissue PA variant (deltal-44,N103,R210,A211,R212,R213,E275,I277).
                                                                                                   Human tissue
US5385732-A.
                                                                                                             AAR70889 standard; protein; 483 AA.
Human tissue PA variant (deltal-44,N103,
                                                                                                                                                                                                                                                                                                                                                                                     AAR70887 standard; protein; 483 AA.
Human tissue PA variant (deltal-44,N103,
                                                                                                                                                                   GETH ) GENENTECH INC.
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                                                                                                                                                                                                                                                                                                                                                                             Human tissue
US5385732-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR70886 standard; protein;
                                                                                          31-JAN-1995
                                                                                                                                                                                                                                                                                                            AAR70881 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human tissue
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                                                                             (GETH ) GENENTECH INC.
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) GENENTECH INC.
7.3%;
21-v 23.4%;
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                                                                                                                                                                                                                                                                                               ndard; protein; 483 AA.
PA variant (deltal-44,N103)
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PA variant (delta1-44,N103,S184,E275,I277)
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No. 1.4e-07;
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No. 1.
                                                                                                                                                                                                                                                                                               , R210, A211, R212, R213, E275).
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                                                                                                              , R252, E275,
                                                                                                                                              DB 2;
.4e-07;
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.4e-07;
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.4e-07;
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.4e-07;
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Best Local Similarity RESULT 1205
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RESULT 1213
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Best Local Similarity
RESULT 1212
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Best Local Similarity
RESULT 1211
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RESULT 1207
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RESULT 1206
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RESULT 1209
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Human t-PA variant
US5385732-A.
                                                                                                                                                                                                                                                                           AAM52182 standard;
Human FVII mutant I
WO200158935-A2.
                                                                                                                                                                                                                                                                                                                                                            AAR70892 standard;
Human t-PA variant
US5385732-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAR70907 standard;
Human t-PA variant
US5385732-A.
Human factor VII
WO2004110469-A2.
23-DEC-2004.
                   ADV44715 standard; protein; 406 AA. Human factor VII mutant K143N/N145T.
                                                                                                       Human factor VII
WO2004029091-A2.
                                                                                                                           ADO10589 standard;
                                                                                                                                             (NOVO) NOVO NORDISK AS.

TY Match 7.3%;
T Local Similarity 23.0%;
                                                                                                                                                                                        ADJ56073 standard; protein; Human factor VII polypeptide WO2004000366-A1.
                                                                                                                                                                                                                                                                                                                                      31-JAN-1995.
(GETH ) GENENTECH INC.
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(GETH ) GENI
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US5385732-A.
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Human tissue PA variant (del
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR70890 standard; protein; 483 AA.
Human tissue PA variant (deltal-44,N103,K210,E275,I277).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31-JAN-1995
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                                                                       MAXY-) MAXYGEN APS.

MAXY-) MAXYGEN HOLDINGS LTD.
                                                  Similarity
                                                                                                                                                                                                                                                      MAXYGEN APS
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                                                                                                                                                                                                                                                                                    ; protein; 406 AA.
K143N/N145T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein; 527 AA.
(N103,A460,A462)
                                                                                                                                                                                                                                                                                                                                                                       protein; 527 AA. (N103, A283, A287)
                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein; 527 (N67,N103).
                                                                                                                                                                                                                                                                                                                    7.3%;
23.4%;
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23.1%;
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                                                                                                                 protein
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(deltal-44,N103,K213,E275)
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e mutant
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Pred. No. 1
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No. 1.
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No. 1.3e-07;
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                                                   1.3e-07;
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.4e-07;
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.6e-07;
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Best Local Similarity RESULT 1214
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                                                                                                                                                                                                                                                            Human tPA variant N103.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADG83826 standard; protein; Brown snake venom protease. WO2003082914-A1.
                                                                                                                                                                                                                                                                                                                                             AAR44816 standard;
Human tPA variant
US5270198-A.
                                                                                                                                                                                                                                                                                                                                                                                                                              AAR14486 standard; protein;
Delta (466-470) tPA variant
WO9113149-A.
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Human Factor VII variant pol
       AAR70900 standard;
Human t-PA variant
                                                                                 Human t-PA variant
US5385732-A.
                                                                                                                                                                               AAR70868 standard;
Human t-PA variant
                                                                                                                                                                                                                                                                                                                                                                                                                     05-SEP-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (NOVO) NOVO NORDISK HEALTH CARE AG.
ry Match 7.3%; Score 286.
t Local Similarity 23.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ĀBFI5046 standard; protein; 406 AA.
Variant human coagulation Factor VII protein #15
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                                                                                                       AAR70860 standard;
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JS5385732-A.
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(N67,N103)
                                                                                                                                                                             protein; 527 AA. (N67, A432, A434).
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23.2%;
        protein; 527 (N103, A410).
                                                                                           protein; 527 AA
(N67, A331, A332)
                                                                                                                           7.2%;
23.2%;
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23.2%;
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23.0%;
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22.2%;
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23.0%;
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polypeptide
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; Score 286.5;
; Pred. No. 1.3
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with
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                  527
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h Y67N
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No. 1.3e-07;
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1.7e-07;
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                                                                                                                           DB 2;
.8e-07;
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.8e-07;
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.8e-07;
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                                        -07;
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Query Match
Best Local Similarity
RESULT 1224
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ID AA
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Best Local Similarity
RESULT 1229
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Sequence of tissue
68).
                                                                                                                                           AAR09270 standard; protein;
t-PA variant H331A, H332A.
                                                                                                                                                                                                                                                                                                                                                                                                                                     /P03061465 ...
18-MAR-1991.
(FUJI ) FUJISAWA PHARM CO LTD.
7.2%; Score
22.1%; Pred.
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T-PA with -ve charged finger and/or kringle domain
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                                                                                                                                                                                                                Sequence of tissue WO8911531-A.
                                                                                                                                                                                                                                                                                                              AAP70880 standard; protein; 527 AA. Thrombolytic proteins 1-9-1-11 having replaced and containing a modified
                                                                  t-PA variant
                                                                            AAR09278 standard;
                                                                                                                                                                                                                                                                                                                                                                      28-DEC-1989.
(BRBI-) BRIT BIO-TECHN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAP70449 standard;
                                                                                                                   (GETH )
                                                                                                                                                                                                                                   AAP91683 standard;
                                                                                                                                                                                                                                                                                                                                                                                           WO8912681-A.
                                                                                                                                                                                                                                                                        (GEMY ) GENETICS INST INC. (LARS/) LARSEN G R.
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 standard; protein;
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                                                                                                                                                                                                                      protein; 527
plasminogen a
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plasminogen activator
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                                                                                           7.2%;
23.2%;
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23.0%;
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23.2%;
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23.1%;
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23.3%;
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22.9%;
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No. 1.
                   285; DB 2;
No. 2e-07;
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No. 1.9e-07;
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No. 2e-07;
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N-linked
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2e-07;
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.9e-07;
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.8e-07;
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RESULT 1233
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RESULT 1239
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RESULT 1238
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RESULT 1237
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OS-OCT-1989

(GETH ) GENENTECH INC.

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Modified human tiss
EP238304-A.
AAR44809 standard;
Human tPA variant
US5270198-A.
                                                                                                                                                                                                                                 Human diagnostic and WO2004023973-A2. 25-MAR-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB11710 standard; protein;
Human serine protease BSSP5
WO200031243-A1
                                                                               Human tissue
US5385732-A.
                                                                                       AAR70844 standard; protein; 483 AA.
Human tissue PA variant (deltal-44,N67
                                                                                                                                                                     AAR70851 standard; protein; 483 AA.
Human tissue PA variant (deltal-44,N67,D184,E275,
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                                                                                                                                                             US5385732-A.
                                                                                                                                                                                                                       (INCY-) INCYTE CORP.
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                                                            (GETH )
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tissue plasminogen
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28.0%;
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23.4%;
          protein;
(N65, S67)
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21.9%;
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23.1%;
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23.1%;
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19.5%;
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19.5%;
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23.0%;
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eutic pprotein
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(hBSSP5)
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No.
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No. 2.
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No. 2.9
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No. 2.1e-07;
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. 2e-07;
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2e-07;
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2.1e-
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.1e-07;
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Best Local Similarity
RESULT 1241
ID AAR70908 standard; p
DE Human t-PA variant (
PN US5385732-A.
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RESULT 1245
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                              RESULT 1249
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RESULT 1246
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Sequence of tissue
WO8912681-A.
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Human t-PA variant
US5385732-A.
                                                                              ABB80068 standard;
Human coagulation f
WO200183725-A1.
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Human t-PA variant
US5385732-A.
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US5385732-A.
ABG73125 standard;
Human coagulation |
WO200277218-A1.
                                                                                                                                                                          AAR23807 standard; protein;
t-PA (Tyr 297) mutant.
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                                                                                                                                                                                                                                                                                                                                                                 AAP70474 standard;
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                                                                       08-NOV-2001
                                                                                                                       (TEXA ) UNIV TEXAS SYSTEM.

ry Match 7.2%;
t Local Similarity 23.2%;
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7.2%;
Similarity 23.1%;
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                                      O NORDISK AS.
7.2%;
ilarity 22.7%;
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        protein; 406 AA. Factor VII mutant
                                                                                         protein; 406 AA. factor VII mutant
                                                                                                                                                                                                                                                        protein; 562
plasminogen a
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(N103,A296,A297,
                                                                                                                                                                                                                                                                                                                                                     protein; 562
plasminogen
                                                                                                                                                                                                                                                                                                                                                                                                                                      protein; 527 (N103, A267).
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23.7%;
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No. 2.3e-07;
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No. 2.4e-07;
                                                                                                                                                                                                                                                                                          284; DB 1;
No. 2.4e-07;
       polypeptide
                                                                                         L305V/M306D/D309S
                                                                                                                                                                                                                                                                                                                                                     analogue
                                      1.9e-07;
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.3e-07;
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.3e-07;
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t-PA variant E303A, R304A.

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Best
RESULT
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RESULT 1253
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                             Query Match
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                                                                                                                                                                                                                                                                                                                                              AAR13917 standard; peptide;
Delta (466-470) tPA variant
                                                                                                                                                                                                                                                                                                                                                                                                                                ADE83543 standard; protein; Rat Protein NP_058839, SEQ | WO2003016475-AZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human factor VII polypeptide WO2004000366-A1.
                                                                    AAR09257 standard; protein;
t-PA variant d1-44, N184D,
                                                                                                                                                         WO2004111242-A1.
                                                                                                                                                               ADW20190 standard; protein; 407
Human factor VII (FVII) protein
                                                                                                                                                                                                                                         Tissue plasminogen
WO8907146-A.
                                                                                                                                                                                                                                                             AAP90169 standard;
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                                                                                                                                                                                                                                                                                                                                      substitutions.
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Human factor VII mutant L305V/M306D/D309S
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TY Match 7.
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                                         (GETH )
                                                                                                                         (MAXY-) MAXYGEN HOLI
(MAXY-) MAXYGEN APS.
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                                                                                                                                   HOLDINGS LTD
                                                                                                                                                                                                                                                  peptide; 5 activator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein;
                                                                                                                                                                                              rics inc.
7.2%;
22.4%;
                                                                                                                                                                                                                                                                                 7.2%;
22.8%;
                                                                                                                                                                                                                                                                                                                                                                              7.2%;
22.8%;
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22.7%;
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                                                                                                    7.2%;
22.2%;
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7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          H CARE AG.
; Score 283.5;
; Pred. No. 1.9
                                                                  483 AA.
I210R, G211A,
                                                                                                                                                                                                                                                                                                                                                                                                                                           482 AA.
ID NO 11161.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                406 AA.
le mutant
                                                                                                                                                                                                                                                             571
527
                                                                                                                                                                                                                                                                                                                                              522 AA.
with K296A,
                                                                                                                                                                                               Score
Pred.
                                                                                                                                                                                                                                                  mutant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score
Pred.
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Pred.
                 Score
Pred.
                                                                                                    Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                              Score
Pred.
                                                                                                                                                                                                                                                                                 Score 283.5;
Pred. No. 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 283.5; DB 9
Pred. No. 1.9e-07;
                                                                                                                                                                AA.
variant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                283.5;
No. 1.9
                                                                                                                                                                                                                                                                                                                                                                              No. 2.
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No.
                  283;
No. 2
                                                                                                                                                                                                283
No.
                                                                                                    283; DB 9;
No. 2e-07;
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                                                                                                                                                                                                                                                   2G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             #21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1.5; DB 6;
1.9e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ٠.
ت. ا
                                                                                                                                                                 sequence
                                                                                                                                                                                                                                                                                                                                              H297A, R298A and R299A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; DB 8;
                                                                                                                                                                                                ; DB 1;
                                                                                                                                                                                                                                                                                                                                                                              ; DB 7;
                   DB 2;
                                                                                                                                                                                                                                                                                  ; DB 2;
.4e-07;
                                                                     K212R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
                                                                                                            Length
                          Length
                                                                     V213R,
                                                                                                                                                                                                                                                                                                                                                                                       Length
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                             483;
                                                                                                               407;
                                                                     T252R,
                                                                                                                                                                                                                                                                                                                                                                                        482;
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                                                                     F305H
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Best Local Similarity
RESULT 1267
                                                                                                                                                     RESULT 1265
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                                                                                                                                                                                                                                                                                                           Best Local Similarity RESULT 1263
                                                                                                                                                            Query Match
Best Local 9
                   Query Match
                                                                                              Query Match
                                                                                                                                                                                                                                         Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human tPA variant
                                                                                                                                                                                                   AAR12367 standard; protein; 561 AA. T-PA with -ve charged finger and/or JP03061483-A.
                                                                                                                                                                                                                                                                               T-PA variant contg. JP03061482-A.
                                                                                                                        Human corin prot
WO2004111225-A1.
                                                                                                                                                         18-MAR-1991.
(FUJI) FUJISAWA PHARM CO LTD.
7.2%; Score
22.1%; Pred.
                                                                                                                                                                                                                                                                                                  AAR12341 standard; protein; 560
                                                                                                                                                                                                                                                                                                                                                          Human t-PA variant
US5385732-A.
                                                                                                                                                                                                                                                                                                                                                                                                                  14-DEC-1993.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR44814 standard;
Human tPA variant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR44817 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR44810 standard;
                                                       Factor VII/IX fusion
                                                                                                                                          ADW42867 standard; protein; 925
                                                                                                                                                                                                                                                                                                                                                                              AAR70899 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human tPA variant
US5270198-A.
                                              WO2006018204-A1.
                                                                 AEG02852 standard;
                                                                                                                                                                                                                                                            (FUJI ) FUJISAWA PHARM CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                       JS5270198-A.
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                                                                                   Local Similarity
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                                                                                                      SCHERING AG
                           ZLB BEHRING
                                                                                                                                  protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein;
(N67, A296,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein; 5 (N65, T67).
                                                                                                                                                                                                                                                                                                                                                                                                                                               protein; 527 (N105, T107).
                                                                 protein;
                                                                                                                                                                                                                                                                                                                                                                   protein; 527 (N103, A408).
                          GMBH.
                                                                                                                                deletion region
                                                                                                                                                                                                                                        7.2%;
22.1%;
                                                                                                                                                                                                                                                                                         fibronectin
                                                                                                                                                                                                                                                                                                                    7.2%;
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23.7%;
        7.2%;
                                                                                   7.2%;
20.5%;
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23.6%;
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23.4%;
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23.1%;
                                                       protein
                                                      436 AA.
n SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               527
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,A297,A298,A299)
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Pred.
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Pred.
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No.
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No.
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No. 2.
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        282.5; DB 1
No. 2.3e-07;
                                                                                   283; DB 9;
No. 4.4e-07;
                                                                                                                                                              283;
No. 2.
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No. 2.
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No. 2
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.6e-07;
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.6e-07;
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.6e-07;
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.7e-07;
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.7e-07;
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                  Length
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                                                                                                                                                                                                                                                                                         (3)
                                                                                                                                                                                                                                                                                                                                                                                                           527;
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AEG02835 standard; peptide; 436 AA. Factor VII/IX fusion protein SEQ II

SEQ ID NO:29

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Query Match
Best Local S
RESULT 1273
                                                                                                                Query Match
Best Local Similarity
RESULT 1275
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                                                                                                                                                                     AAR09255 standard; protein; t-PA variant I210R, G211H, WO9002798-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR09246 standard; protein; 483 AA. t-PA variant d1-44, N184D, F305H. W09002798-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADW20177 standard; protein; 406 Human factor VII (FVII) protein W02004111242-A1.
                                                                                                                                                                                                                                                                                                                                                            AAR09254 standard; protein; 483 AA.
L-PA variant d1-44, I210R, G211H, K212Q, V213K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AEL92410 standard; protein; 406 A/Human Factor VII protein variant, W02006114105-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR09231 standard; protein; 524 t-PA deletion variant d297-299.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO2006018204-A1
                                                                             tPA variant
WO9202612-A.
                                                                                       AAR21600 standard; protein; 527
tPA variant - E94A, D95A, T103N
                                                                                                                                                                                                                                                                      AAR09230 standard; protein; 525
t-PA deletion variant d297-298.
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 AAR70866 standard;
Human t-PA variant
                                                                                                                                                                                                                                                                                                                                          22-MAR-1990.
                                                                                                                                                                                                                                                                                                                              (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                22-MAR-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (MAXY-) MAXYGEN HOLDINGS LTD
                                                                                                                                                 22-MAR-1990
(GETH ) GENI
                                                                                                                                                                                                                                        (GETH )
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                                Local Similarity
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protein; 527 AA. (N67, A416, A417, A418).
                                7.1%;
23.2%;
                                                                                                                         7.1%;
22.8%;
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23.4%;
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23.0%;
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22.8%;
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22.3%;
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24.2%;
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22.1%;
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22.8%;
                                                                                                                                                                            , 527 AA.
K212Q, V213K,
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Pred.
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Pred.
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Pred.
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Pred. No. 2.3e-07;
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Pred. No. 2
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No. 2
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No. 2
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No. 2.7e-07;
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                                 Ν
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2.3e-07;
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.9e-07;
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.7e-07;
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.3e-07;
                                DB 2;
.9e-07;
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.9e-07;
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                                                                                                                                                                                                                                                                                                                   483;
                                            527;
                                                                                                                                    527;
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Best Local Similarity
RESULT 1277
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 Best Local Similarity
RESULT 1285
ID AAO30584 standard;
DE Human coagulation f
                                                                                                                                                                                                Query Match
Best Local Similarity
RESULT 1283
                                                                                                                                                                                                                                                                                     Best Local Similarity RESULT 1282
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                                                                                                            Best Local Similarity
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                                              Query Match
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Human t-PA variant (
US5385732-A.
31-JAN-1995.
(GETH ) GENENTECH IN
                                                                                                                                                                                                                                                                                                                                                                             28-DEC-1989.
28-DEC-1989.
(BRBI-) BRIT BIO-TECHN LTD.
7 1%;
21Y Match 7 1%;
23.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                            AAR09287 standard;
Sequence of tissue
WO8912681-A.
                                                                                                                                                               AAB84869 standard; protein; 406 AA.
Mutant blood coagulant factor VII (FVII-30)
JP2001061479-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAP82582 standard;
Tissue plasminogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31-JAN-1995.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR70869 standard;
Human t-PA variant
US5385732-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31-JAN-1995.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                t-PA (Gly
                                                                                                                                                                                                                                                                        AAR23810 standard; protein;
                                                                                      AAM52185 standard;
Human FVII mutant (
                                                                                                                                                                                                                            16-APR-1992.
(TEXA ) UNIV TEXAS SYSTEM
                                                                                                                                                                                                                                                      WO9206203-A.
                                                                                                                                                                                                                                                                                              (TEXA) UNIV TEXAS SYSTEM.

ry Match 7.1%;
t Local Similarity 23.5%;
                                                                                                                                                                                                                                                                                                                                           WO9206203-A
                                                                                                                                                                                                                                                                                                                                                              AAR23808 standard; protein;
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                                                                                                                                           ZH KAGAKU &
                                                                                                                                                                                                                                                                301) mutant.
                                                                                                                                                                                                                                                                                                                                                    298) mutant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INC.
protein; 406 AA. factor VII variant (S314E/L305V/V158D/K337A/M298Q).
                                                                                       g291N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein; 52 (N67, A440).
                                                                                                                                                                                                                                                                                                                                                                                                                                      protein; 562 AA.
plasminogen acti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein; 562 AA. activator with S-119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein; 527 AA.
(N103,A426,A427,A429,A430)
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7.1%;
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Human factor VII protein mutant
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Human factor VII/VIIa protein mu
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Human factor VII mutant S314B/L305V/V158T/K337A/M298Q.
W02004110469-A2.
23-DEC-2004.
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Human factor VII mutant K316Q/L305V/V158T/K337A/M298Q.
WO2004110469-A2.
23-DEC-2004.
(NOVO ) NOVO NORDISK AS.
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Human factor VII mutant
WO2004110469-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADV44568 standard; protein; 406 AA. Human factor VII mutant S314E/L305V/V158D/K337A/M298Q. WO2004110469-A2. 23-DEC-2004.
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30-SEP-2004.
                                                                ADV44556 standard; protein; 406 AA.
Human factor VII mutant S314E/L305V/K337A/M298Q.
WO2004110469-A2.
23-DEC-2004.
                                                                                                                                                            ADV44673 standard;
Human factor VII mu
WO2004110469-A2.
                                                                                                                                                                                                                                     ADV44612 standard; protein; 406 AA.
Human factor VII mutant K316Q/L305V/V158D/K337A/M298Q.
WO2004110469-A2.
23-DEC-2004.
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(NOVO) NOVO NORDISK AS.
(Ty Match 7.1%;
The Local Similarity 22.5%;
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ry Match 7.1%;
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ry Match 7.1%;
t Local Similarity 22.5%;
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             ADV44704 standard;
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d; protein; 406 AA.
mutant F374Y/V158T/S314E/M298Q/K337A/L305V.
                                                                                                                                                                     d; protein; 406 AA.
mutant F374Y/L305V/M298Q/K337A/S314E
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utant F374Y/V158D/M298QV/S314E/K337A/L305V.
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.4e-07;
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.4e-07;
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Best Local Similarity
RESULT 1313
ID ADV44600 Stand
DE Human far'
PN WO200
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Best Local S
RESULT 1316
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RESULT 1314
ID ADY74145 standard; protein;
DE Human Factor VII variant pol
PN WO2005024006-A2.
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RESULT 1317
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RESULT 1318
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23-DEC-2004.
(NOVO ) NOVO NOR
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Human Factor VII ve
WO2005024006-A2.
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Human factor VII mutant K316Q/L305V/K337A/M298Q.
                                                                                       ADY74308 standard; protein; 406 AA. Human Factor VII variant polypeptide W02005024006-A2.
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Ty Match
Ty 11, Score 281.5; DB 9;
L Local Similarity
22.5, Pred. No. 2.4e-07;
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ry Match 7.1%;
t Local Similarity 22.5%;
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(NOVO ) NOVO
ADY74201 standard;
Human Factor VII ve
WO2005024006-A2.
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17-MAR-2005.
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Human Factor VII variant polypeptide
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ry Match 7.1%; Score
t Local Similarity 22.5%; Pred.
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h 7.1%;
Similarity 22.5%;
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         1; protein; 406 AA. variant polypeptide
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polypeptide
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Score 281.5; DB 9
Pred. No. 2.4e-07;
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                                                                                                       Variant human coagulation Factor VII W02005123916-A2.
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"Y Match 7.1%; Score 281.5;
t Local Similarity 22.5%; Pred. No. 2.
Variant human coagulation WO2005123916-A2.
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Ty Match 7.1%; Score 2
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ry Match 7.1%; Score 281.
t Local Similarity 22.5%; Pred. No.
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Human Factor VII variant polypeptide
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ry Match 7.1%; Score 281.5;
t Local Similarity 22.5%; Pred. No. 2.4
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Human Factor VII variant polypeptide
                            AEF15157 standard;
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Y Match 7.1%; Score 281.
Local Similarity 22.5%; Pred. No.
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coagulation Factor VII protein #52
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Mation Factor VII
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22.5%;
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Best Local Similarity RESULT 1331
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t-PA variant d1-44, I210R, (
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                                                                                                                           AAR70855 standard; protein; 483 AA.
Human tissue PA variant (deltal-44,N67,K210,E275,I277)
                                                                                                                                                                                               t-PA variant
WO9002798-A.
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T-PA with -ve charged finger and/or
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US5385732-A.
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WO2004111242-A1.
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                              US5385732-A
31-JAN-1995
                                                AAR70845 standard; protein; 483 AA.
Human tissue PA variant (deltal-44,N67,S184,E275)
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(GETH ) GENE
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                      GETH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AR13919 standard;
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Match 7.1%; Score
Occal Similarity 21.9%; Pred.
                                                                                                ) GENENTECH
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7.1%; Score 281.
                   GENENTECH
                                                                                                                                                                           GENENTECH INC.
                                                                                                                                                                                                                                    Similarity
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                                                                                                                                                                                                                                                                  HOLDINGS LTD
                                                                                                                                                                                                                                                                                               i; protein; (FVII) prot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein;
A variant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein;
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ant d297-301.
7.1%;
23.2%;
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23.2%;
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23.3%;
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22.2%;
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23.2%;
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22.7%;
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23.4%;
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d300-302.
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with E426A,
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1 variant
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No. 3
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No. 2.
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No. 3e-07;
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; DB 2;
3e-07;
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3e-07;
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                                                                                                                                                                                                                                                                                                                                                                                                       .5; DB 2;
3.1e-07;
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3.1e-07;
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                                                                                                                                                                                                                                                                                               sequence
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.4e-07;
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                                                                                      483;
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AAR70848 standard;

tissue

PA

rd; protein; variant (de:

in; 483 AA. (deltal-44,N67,R252,E275).

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Query Match
Best Local Similarity
RESULT 1340
                                    Best Local Similarity RESULT 1348
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Best Local Similarity
RESULT 1346
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Best Local Similarity
RESULT 1344
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                                                                                                                                                                                                                                                                                             Human tissue US5385732-A.
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US5385732-A.
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Human tissue PA variant (deltal-44,N67,K210,E275)
Human tissue
US5385732-A.
                     AAR70853 standard; protein;
                                                                                                           Human tissue
                                                                                                                                                                                                                                                                                                      AAR70850 standard; protein; 483 AA.
Human tissue PA variant (deltal-44,N67,E275,I277)
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US5385732-A.
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US5385732-A.
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US5385732-A.
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Human tissue PA variant (deltal-44,N67,E275).
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US5385732-A.
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Human tissue PA variant (deltal-44,N67,R252,E275,
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                                                                                              US5385732-A.
                                                                                                                      AAR70847 standard;
                                                                                                                                                                                                           Human tissue
                                                                                                                                                                                                                       AAR70852 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                    AAR79144 standard; protein;
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Human tissue PA variant (deltal-44,N67,K213,E275)
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PA variant (del
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        rd; protein; 483 AA.
variant (delta1-44,N67,R210,A211,R212,R213,E275,I277).
                                                                                                       rd; protein; 483 AA. variant (deltal-44,N67,R210,A211,R212,R213,
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23.2%;
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23.28;
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23.2%;
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23.0%;
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No. 3e-07;
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No. 3e-07;
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No. 3e-07;
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No. 3e-07;
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Best Local Similarity RESULT 1350
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                             Query Match
Best Local Similarity
RESULT 1357
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Best Local Similarity
RESULT 1356
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RESULT 1353
ID AAB70411 standard;
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Best Local Similarity
RESULT 1351
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                                                                                                                                                  t-PA deletion variant d300-301. W09002798-A.
                                                                           AAR09276 standard; protein;
t-PA variant K416A, H417A, I
WO9002798-A.
                                                                                                                                                                                                                                                                                                    Human factor X protein sequence SEQ WO200110896-A2.
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Human Factor X protein.
WO9838317-A1.
                                                                                                                                                                                                                                AAR60502 standard; protein;
Serine protease for fusion protease.
                                                                                                                                                                                                                                                                                                                                                                                             AAW76218 standard;
Human Factor X prot
AAR09279 standard;
t-PA variant R440A.
WO9002798-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human Factor X protein analogue. WO9838317-Al.
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(IMMO ) IMMUNO AG
                                                           (GETH )
                                                                                                                                                22-MAR-1990
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protein.
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                   protein;
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24.0%;
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protein
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No. 3
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No. 3.1e-07;
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No. 3.1e-07;
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3e-07;
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.3e-07;
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Query Match
Best Local Similarity
RESULT 1358
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Human t-PA variant
US5385732-A.
                                                                                                                                                                                Wild type tissue US5385732-A. 31-JAN-1995.
                       T-PA with -ve charged finger and JP03061483-A.
18-MAR-1007
                                                                                                                                                                                                 AAR70842 standard; protein; !
Wild_type_tissue_plasminogen
                                                                                                                                                                                                                                                                                AAR70872 standard; protein; 527 AA.
Human t-PA variant (N67,A460,A462)
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US5385732-A.
                                                                                                                                                                                                                                                                                                                                                                          AAR70906 standard;
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                                                                                                            JP03061483-A.
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-PA with -ve charged finger
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                                                                                        FUJISAWA PHARM CO LTD.
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             FUJISAWA
PHARM CO LTD.
7.1%; Score
                                                                                                                                                                                                                                                                                                                                                               protein; 527 AA. (N103, A449, A453).
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23.2%;
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and/or
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.3e-07;
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Best Local Similarity
RESULT 1367
ID AAP80691 standard; p
DE Hybrid plasminogen/t
PN EP29226-A.
                               Best Local Similarity RESULT 1375
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(NOVO) NOVO NORDISK AS.
7.1%;
YY Match 7.1%;
YY Local Similarity 22.5%;
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Human coagulation
WO2003037932-A2.
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(BEEC ) BEECHAM GROUP PLC.
7.1%;
Human coagulation WO2003037932-A2.
                                                                                               Human coagulation
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(NOVO ) NOVO NORDISK AS.
                   AAO30606 standard;
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ry Match 7.1%;
t Local Similarity 22.5%;
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factor VII variant (K316H/L305V/K337A/M298Q)
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factor VII variant (S314E/L305V/M298Q)
         protein; 406 factor VII var
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          (K316H/L305V/V158D/K337A/M298Q)
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Best Local Similarity

NOVO NORDISK

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280.5; DB 6 No. 2.8e-07;

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Human coagulation;
WO2003037932-A2.
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                                                                                                                    ADJ55965 standard;
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WO2004000366-A1.
31-DEC-2003.
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Human factor VII polypeptid
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Human factor VII polypeptide
WO2004000366-A1.
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08-MAY-2003.
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WO2004000366-A1.
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Best Local Similarity RESULT 1391
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WO2004000366-A1.
31-DEC-2003.
(NOVO ) NOVO NORDI
                                                                                                                                                                                                                                                        ADJ56016 standard; protein; Human factor VII polypeptide WO2004000366-A1.
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Human factor VII polypeptide
WO2004000366-A1.
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Human factor VII po
WO2004000366-A1.
                                         ADJ56056 standard;
Human factor VII pc
WO2004000366-A1.
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Human factor VII polypeptide
WO2004000366-A1.
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Human factor VII polypeptide mutant
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WO2004000366-Al.
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ry Match 7.1%;
t Local Similarity 22.5%;
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(NOVO ) NOVO NORDISK
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                                   ADY74285 standard; protein; 406 AA. Human Factor VII variant polypeptide WO2005024006-A2.
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Human factor VII mutant K316H/L305V/K337A/M298Q
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WO2004110469-A2.
                                                                                 (NOVO ) NOVO NORDISK HEALTH
ry Match 7.1%;
t Local Similarity 22.5%;
                                                                                                              ADY74113 standard; protein; 406 AA. Human Factor VII variant polypeptide WO200502406-A2.
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Human factor VII (FVII) protein
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Human factor VII m
WO2004110469-A2.
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Human factor VII mutant K31
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Human factor VII ()
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WO2004110469-A2.
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mutant K316Q/L305V/V158D/M298Q
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(FVII) protein variant
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7.1%;
ery Match 7.1%;
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Human Factor VII variant pol
W02005024006-A2.
17-MAR-2005.
(NOVO ) NOVO NORDISK HEALTH
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Human Factor VII ve
WO2005024006-A2.
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Human Factor VII variant polypeptide
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ry Match 7.1%; Score 280.
t Local Similarity 22.5%; Pred. No.
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Human Factor VII va
                                                                    ADY74103 standard; protein; 406 AA.
Human Factor VII variant polypeptide
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Human Factor VII variant pol
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ry Match 7.1%;
t Local Similarity 22.5%;
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17-MAR-2005.
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Human Factor VII variant polypeptide
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ry Match 7.1%;
t Local Similarity 22.5%;
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Human Factor VII variant polypeptide #135.

W02005024006-A2.

17-MAR-2005.

10NOVO ) NOVO NORDISK HEALTH CARE AG.

(NOVO ) NOVO NORDISK HEALTH CARE AG.

T.1%; Score 280.5; DB 9;

IL Local Similarity 22.5%; Pred. No. 2.8e-07;
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                                                                  AEF15119 standard; protein; 406 AA.

Variant human coagulation Factor VII protein #88.

W02005123916-A2.

29-DEC-2005.

(NOVO ) NOVO NORDISK HEALTH CARE AG.

(NOVO ) NOVO NORDISK HEALTH CARE AG.

7.1%; Score 280.5; DB 10.

11 Local Similarity 22.5%; Pred. No. 2.8e-07;
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(NOVO ) NOVO NORDISK HEALTH CARE AG.
(NOVO ) NOVO NORDISK HEALTH CARE AG.
7.1%; Score 280.5; DB 9;
"Toral Similarity 22.5%; Pred. No. 2.8e-07;
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(NOVO ) NOVO NORDISK HEALTH CARE AG.

(NOVO ) T.1%; Score 280.5; DB 9;

T. G.Cal Similarity 22.5%; Pred. No. 2.8e-07;
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1.18; Score 280.5; DB 9;

1.18 Score 280.5; DB 9;

22.58; Pred. No. 2.8e-07;
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Human Factor VII variant pol
WO2005024006-A2.
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(NOVO) NOVO NORDISK HEALTH CARE AG.
7.1%; Score 280.5; DB 9;
t Local Similarity 22.5%; Pred. No. 2.8e-07;
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L Local Similarity 22.5%; Pred. No. 2.8e-07;
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t Local Similarity 22.5%; Pred. No. 2.8e-07;
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Local Similarity 22.5%; Pred. No. 2.8e-07;
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NEF15089 standard; protein; 406 AA.
Variant human coagulation Factor VII protein #58.
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polypeptide #187.
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.8e-07;
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요합하다	RESULT 144 ID AEF15 DE Varia PN WO200 PD 29-DE PA (NOVO	ID AEP DE Var PN WO2 PD 29-I PA (NO) Query I Best La	1 V 9-	S B &	SGE	S B C	a Bro	SE O	WO29- 29- (NC Query Best I
tch als als fac fac	7 144 nt h 5123 5-20 C-20	123 123 -20 N	77 1123 123 1 S	SOSP	AEF15136 stand Variant human WO2005123916-J 29-DEC-2005. (NOVO) NOVO 1 ery Match Ery Match LT 144 at an AEF15134 standard limits with the control of the co	ABF15146 stan Variant human W02005123916-, 29-DEC-2005. (NOVO) NOVO: (NOVO) NOVO: st Local Simil	99 t h 123 -20 -20 N Ch	73 123 -20 N Ch	15, 712
larit ndard VII -A1.	idard; i coagu A2.	ndard; 1 coagu .A2. NORDIS	indard; in coagu ;-A2. NORDIS	NORDIS	ndard; n coagu -A2. NORDIS	ndard; n coagu .A2. NORDIS	ndard; 1 coagu A2. NORDIS	standard; pr human coagula 3916-A2. 005. NOVO NORDISK	3916-A2. 005. NOVO NORDISK Similarity
7.1%; 22.5%; rotein; II) prot	tein; ion Fa	crotein; lation Fa lation Fa (HEALTH 7.1%; 22.5%;	protein; lation Fa K HEALTH 7.1%; 22.5%;	HEALTH 7.1%; 22.5%;	protein; lation E lation E K HEALTH 7.1%; 22.5%;	protein; lation Fa K HEALTH 7.1%; 22.5%;	protein; lation Fa K HEALTH 7.1%; 22.5%;	ntion Fa tion Fa HEALTH 7.1%; 22.5%;	HEALTH 7.1%; 22.5%;
d. N AA. vari	6 AA. or VI	actor VII CARE AG. Score 28 Pred. No	actor VII CARE AG. Score 28 Pred. No	CARE AG. Score 28 Pred. No	VIII AG. re 2 d. N	406 AA. ctor VII CARE AG. Score 28 Pred. No	406 AA. Ictor VII CARE AG. Score 28 Pred. No	406 AA. cctor VII CARE AG. Score 28 Pred. No	CARE AG. Score 280 Pred. No.
0.5; D . 2.8e- nt sequ	protein	protein 0.5; D	protein 0.5; D	protein 0.5; D	protein 0.5; D	protein 0.5; D	protein 0.5; D	protein 0.5; D	0.5; D
B 10; L 07; ence #31	# #	#55. B 10; 07;	#46. B 10; 07;	#103. B 10; 07;	#105. B 10; 07;	#115. B 10; 07;	#68. B 10; 07;	#42. B 10; 07;	B 10;
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26-JUN-2003.

(ELIL) LILLY & CO ELI.

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MARICH 77-(EY 21.9%;
                   27-MAY-1993.
(SCHA/) SCHAFFER
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(MAXY-) MAXYGEN
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Human factor VII (FVII) protein
W02004111242-A1.
23-DEC-2004.
(MAXY-) MAXYGEN HOLDINGS LTD.
(MAXY-) MAXYGEN APS.
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Sequence of tissue
EP242836-A.
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                                                Factor X.
WO9309803-A1.
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Human factor VII (I
WO2004111242-A1.
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WO2003052059-A2.
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Bovine recombinant
                                                                    AAR37402 standard;
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(FVII) protein
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7 21.9%;
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plasminogen activator
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No. 3.7e-07;
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4.2e-07;
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RESULT 1465
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T-PA deriv. (V).
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                                                                                                                                                                                                                                                                                                                       AAR09267 standard; protein;
t-PA variant D283A, H287A.
                                                                                                                                                                                                                                                                                                                                                                                                      AAR05488 standard; protein; tPA024 precursor protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR09245 standard; protein;
t-PA deletion variant d297,
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                                                                                                                                                                                                                                                  t-PA variant
                                                                                                                                                                                                                                                    AAR09282 standard;
t-PA variant D460A,
                                                                                                                                                                                                                                                                                                                                                                                              tPA024 precursor
EP373896-A.
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Modified FVII-UAA-GPI cassette.
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(UNIW ) UNIV WASHINGTON.
                            EP445464-A.
                                    AAR13912 standard;
T-PA deriv. (III).
                                                                                                 EP445464-A.
                                                                                                                                                                       EP445464-A.
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(GETH ) GENENTECH
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23.0%;
KAGAKU KOGYO KK.
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Best Local Similarity RESULT 1470
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JP03285680-A.
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L6-DEC-1991.
(SUMU ) SUMITOMO SEIYAKU KK.
(SUMU ) 7.1%;
FIY Match 7.1%;
23.0%;
                                                                                                            t-PA analogue
JP03285680-A.
                                                                                                                                                                                          AAR20222 standard; protein;
t-PA analogue expressed by p
                                            AAR44811 standard; protein;
Human tPA variant N67.
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pCDM8-014.
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pCDM8-013.
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Single chain form WO9802454-A2.
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W09821320-A2.
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US5385732-A.
                                                                                                           Recombinant
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WO200243747-A2.
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                                         AAP80655 standard; |
Tissue plasminogen |
EP293934-A.
07-DEC-1988.
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Sequence of active
EP178105-A.
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Sequence of human p
GB2173804-A.
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T-PA variant contg.
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T-PA variant contg.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human diagnostic WO2004023973-A2.
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Human diagnostic and therapeutic pprotein
                                                                                                        Tissue plasinogen WO8800242-A. 14-JAN-1988.
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EP143081-A.
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(GETH ) GENENTECH INC.
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(FUJI) FUJISAWA PHARM CO LTD.
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68).
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Sequence of tissue plasminogen
with altered residues 419 and 4
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(KABI ) KAB
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Sequence of tissue plasminogen a
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EP379890-A.
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Novel tissue plasminogen activator
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Sequence of tissue
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JP01174388-A.
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EP351246-A.
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